

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 04:49:48 ; Search time 913 Seconds

(without alignments)
11505.704 Million cell updates/sec

Title: US-09-980-650-6

Perfect score: 2788

Sequence: 1 aaataagatcttactgtctt.....tactagagatcatcatcag 2788

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank

1: gb_da:*

2: gb_hlg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

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28: em_un:*

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31: em_hlg_inv:*

32: em_hlg_other:*

33: em_hlg_mus:*

34: em_hlg_pln:*

35: em_hlg_rod:*

36: em_hlg_mam:*

37: em_hlg_vrt:*

38: em_ey:*

39: em_hugo_hum:*

40: em_hugo_mus:*

41: em_hugo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2788	100.0	2788	6	AX044390 Sequence
2	2659.4	95.4	2692	6	AX044391 Sequence
3	2407.6	86.4	2436	6	AX044392 Sequence
4	2333.2	83.7	2788	6	AX044393 Sequence
5	2204.6	79.1	2692	6	AX044394 Sequence
6	1952.8	70.0	2436	6	AX044395 Sequence
7	1951	70.0	2062	6	AX044385 Sequence
8	1848.2	66.3	7378	6	AR110602 Sequence
9	1848.2	66.3	7378	6	AR151001 Sequence
10	1848.2	66.3	7378	6	AR152424 Sequence
11	1848.2	66.3	7378	6	AR152433 Sequence
12	1848.2	66.3	7378	6	AR184317 Sequence
13	1848.2	66.3	7378	6	AR212558 Sequence
14	1845.4	66.2	1851	6	AR110596 Sequence
15	1845.4	66.2	1851	6	AR150995 Sequence
16	1845.4	66.2	1851	6	AR152418 Sequence
17	1845.4	66.2	1851	6	AR152427 Sequence
18	1845.4	66.2	1851	6	AR184311 Sequence
19	1845.4	66.2	1851	6	AR212552 Sequence
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21	1845	66.2	1845	12	SYNCRVIA
22	1844.8	66.2	3484	6	AR127687 Sequence
23	1844.8	66.2	3484	6	I75356 Sequence 10
24	1843.4	66.1	1845	6	AR029508 Sequence
25	1843.4	66.1	1845	6	AR098461 Sequence
26	1843.4	66.1	1845	6	AX441374 Sequence
27	1843.4	66.1	1845	6	AX453870 Sequence
28	1843.4	66.1	1845	6	I41421 Sequence 5
29	1843.4	66.1	3531	6	AR127585 Sequence
30	1843.4	66.1	3531	6	I75254 Sequence 3
31	1507.8	54.1	2062	6	AX044386 Sequence
32	1409.6	50.6	1857	1	BTCRYDE
33	1392.6	49.9	3478	6	AR127583 Sequence
34	1392.6	49.9	3478	6	I75252 Sequence 1
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37	1220.4	43.8	2815	6	A04444 Synthetic p
38	1220.4	43.8	2815	6	A04445 Synthetic p
39	1220.4	43.8	2815	6	I12419 Sequence 2
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41	1220.4	43.8	3066	6	A04448 Synthetic p
42	1220.4	43.8	3540	1	I12420 Sequence 3
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44	1220.4	43.8	3550	1	BTCRYIAB
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ALIGNMENTS

RESULT 1

AX044390

LOCUS AX044390 2788 bp DNA linear PAT 24-NOV-2000

DEFINITION Sequence 6 from Patent WO0066755.

ACCESSION AX044390

VERSION AX044390.1 GI:11343268

KEYWORDS

SOURCE

ORGANISM

synthetic construct

artificial sequences.

REFERENCE

1

AUTHORS Christou, P. and Mehlo, L.

TITLE Pesticidal fusions

JOURNAL Patent: WO 0066755-A 6 09-NOV-2000;

Plant BioScience Limited (GB)

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      source          location/Qualifiers
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                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
                        /note="Nucleotide sequence of CRYIA(b) RTB1 in pRSTBAC1"

BASE COUNT
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ORIGIN

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Best Local Similarity	100.0%	Pred. No. 0		
Matches 2788	0	Mismatches	0	Gaps 0

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Db	1	AAATPAGATTTTACTGTTTTCGTAAACAGTTTGTGTAATAAAAAAACCTATAATTTCCG	60
OY	61	GATTATTCATCCCGTCCCAACCATCGGGGCGGATCATGGAACAAACCAACATCAAC	120
Db	61	GATTATTCATCCCGTCCCAACCATCGGGGCGGATCATGGAACAAACCAACATCAAC	120
OY	121	GAATGCATTCATACAACTGCTTGAGTAAACCAAGATTGAAGTACTTGTGTGAGAACCC	180
Db	121	GAATGCATTCATACAACTGCTTGAGTAAACCAAGATTGAAGTACTTGTGTGAGAACCC	180
OY	181	ATTGAAACCGGTTAACAATCCCATCGAACAATCTCTGTCTTGACACAGTTTCTGTACG	240
Db	181	ATTGAAACCGGTTAACAATCCCATCGAACAATCTCTGTCTTGACACAGTTTCTGTACG	240
OY	241	GAGTTCGTCCAGAGTGTGGTTCGTTCTCGGACTAGTTGAATCATCATCTGGGGATCTTT	300
Db	241	GAGTTCGTCCAGAGTGTGGTTCGTTCTCGGACTAGTTGAATCATCATCTGGGGATCTTT	300
OY	301	GSTCCATCTCAATGGGATGACATTCCTGGTGCAAATTGACGATGATCAACAGAGATC	360
Db	301	GSTCCATCTCAATGGGATGACATTCCTGGTGCAAATTGACGATGATCAACAGAGATC	360
OY	361	GAAGAGTTTCGCGCAGAGAACGAGCCACTCTAGTGTGGAAGATTGAGCAATCTCAACAA	420
Db	361	GAAGAGTTTCGCGCAGAGAACGAGCCACTCTAGTGTGGAAGATTGAGCAATCTCAACAA	420
OY	421	ATCTATGACAGAGAGCTTTACAGAGATGGGAAAGCCATCTCACTAACCCAGCTCTCCGCGAG	480
Db	421	ATCTATGACAGAGAGCTTTACAGAGATGGGAAAGCCATCTCACTAACCCAGCTCTCCGCGAG	480
OY	481	GAATAGCCTATTCATTCACACGACATGAACAGCGCCTTGACACAGCATCCCATTTGTC	540
Db	481	GAATAGCCTATTCATTCACACGACATGAACAGCGCCTTGACACAGCATTCCTCATTTGTC	540
OY	541	GCAGTCCAGAACTACCAAGTTCTCTCTTGTCCGTGACGTTCAAGCAGCTAATCTTCAAC	600
Db	541	GCAGTCCAGAACTACCAAGTTCTCTCTTGTCCGTGACGTTCAAGCAGCTAATCTTCAAC	600
OY	601	CTCAGCGGCTTCGAGACGTTAGGCGTTTGGGCAAAAGTGGGGATTGGATCTGTCACAC	660
Db	601	CTCAGCGGCTTCGAGACGTTAGGCGTTTGGGCAAAAGTGGGGATTGGATCTGTCACAC	660
OY	661	ATCAATAGCCGTTTACAAAGACCTTACTAGCTGATTGGAAATCAACCGACCAACGCTGT	720
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OY	721	CGTTGGTACAAACATCGGCTTGGAGGGGTGCTTGGGGTCCTGATTTCTAGAGATTGGATTAGA	780
Db	721	CGTTGGTACAAACATCGGCTTGGAGGGGTGCTTGGGGTCCTGATTTCTAGAGATTGGATTAGA	780
OY	781	TACAACCAAGTTACAGAGAAATTTGACCCCTCAAGATTTTGGACATTTGTGCTCTTCCCG	840
Db	781	TACAACCAAGTTACAGAGAAATTTGACCCCTCAAGATTTTGGACATTTGTGCTCTTCCCG	840
OY	841	AACTATGACTCCAGAACTCACTCTATCCGTACAGTGTCCCAACTTACACAGAGAAATCTAT	900
Db	841	AACTATGACTCCAGAACTCACTCTATCCGTACAGTGTCCCAACTTACACAGAGAAATCTAT	900

QY	901	ACTAACCCAGTTCTTGAGAACTTGTGACGGTACGTTCCGTGGTCTTCCGCCAACGATACGAA	960
Db	901	ACTAACCCAGTTCTTGAGAACTTGTGACGGTACGTTCCGTGGTCTTCCGCCAACGATACGAA	960
QY	961	GGCTTCATCAGAGAGCCCACTTGTAGACATCTTGGAAACAGCATATACATCTACACCGAT	1020
Db	961	GGCTTCATCAGAGAGCCCACTTGTAGACATCTTGGAAACAGCATATACATCTACACCGAT	1020
QY	1021	GCTCACAGAGAGATTTACTGGTCTGAGAACCAAGATCATGGCTCTCCAGTTGGAATTC	1080
Db	1021	GCTCACAGAGAGATTTACTGGTCTGAGAACCAAGATCATGGCTCTCCAGTTGGAATTC	1080
QY	1081	AGCGGGCCGAGTTTACCTTCTCTCTCTATGGAACATAAGGAAAACGCGCTCCACAACAA	1140
Db	1081	AGCGGGCCGAGTTTACCTTCTCTCTCTATGGAACATAAGGAAAACGCGCTCCACAACAA	1140
QY	1141	CGTATCGTTGCTCAACTAGAGTCAAGGAGTGCTTACAGAACCTTGTCTTCCACTTGATCAGA	1200
Db	1141	CGTATCGTTGCTCAACTAGAGTCAAGGAGTGCTTACAGAACCTTGTCTTCCACTTGATCAGA	1200
QY	1201	AGACCCCTCATATTCGGATATCAACACAGAACCTTTCGGTCTTGAACGGAAACAGAGTTC	1260
Db	1201	AGACCCCTCATATTCGGATATCAACACAGAACCTTTCGGTCTTGAACGGAAACAGAGTTC	1260
QY	1261	GCTTATGGAACCTCTTCTTCACTTGCATCCGCTGTTTACAGAAAGAGGGAACCGTTGAT	1320
Db	1261	GCTTATGGAACCTCTTCTTCACTTGCATCCGCTGTTTACAGAAAGAGGGAACCGTTGAT	1320
QY	1321	TCCTTGGACGAAATCCCAACCAAGAACAACTATGTCACCCAGGCAAGATTTCTCCAC	1380
Db	1321	TCCTTGGACGAAATCCCAACCAAGAACAACTATGTCACCCAGGCAAGATTTCTCCAC	1380
QY	1381	AGGTTGAGCCACGATGCCATGTCGGTCCGGATTTACAGCAACAGTCCGATAGCATATC	1440
Db	1381	AGGTTGAGCCACGATGCCATGTCGGTCCGGATTTACAGCAACAGTCCGATAGCATATC	1440
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Db	1441	AGAGCTCCTATGTTCTCATGAGATTCAATGATGTCGATGATTCACCAATATCATTTCTTCC	1500
QY	1501	TCTCAAAATCACCCAAATCCCACTTGAACCAAGTCACTACTAATCTTGAATCTGGAATCTGTG	1560
Db	1501	TCTCAAAATCACCCAAATCCCACTTGAACCAAGTCACTACTAATCTTGAATCTGGAATCTGTG	1560
QY	1561	GTGAAGAAGCAGAGCTTCCACAGAGGTGATTTCTTAGAAMAACCTTCTCGGCGAGATT	1620
Db	1561	GTGAAGAAGCAGAGCTTCCACAGAGGTGATTTCTTAGAAMAACCTTCTCGGCGAGATT	1620
QY	1621	AGCAACCTCAGAGTTAATCATCATGCGAACACTTTCTCAAAATATTCGTGTAGAGATTGCT	1680
Db	1621	AGCAACCTCAGAGTTAATCATCATGCGAACACTTTCTCAAAATATTCGTGTAGAGATTGCT	1680
QY	1681	TACGCATCTACCACTTGCATATTCACACCTTCATCGACGGAAGGCTCATCATAG	1740
Db	1681	TACGCATCTACCACTTGCATATTCACACCTTCATCGACGGAAGGCTCATCATAG	1740
QY	1741	GGTAACTTCTCCGCAACCATGTCAAGCGGCAAGCACTTGCATATCCGACGTTCAAGAAC	1800
Db	1741	GGTAACTTCTCCGCAACCATGTCAAGCGGCAAGCACTTGCATATCCGACGTTCAAGAAC	1800
QY	1801	GTCGGTTTCACTACCTCTTTCATCTTCTTAACGGATCAAGCGTTTTCACCCCTTAGCGCT	1860
Db	1801	GTCGGTTTCACTACCTCTTTCATCTTCTTAACGGATCAAGCGTTTTCACCCCTTAGCGCT	1860
QY	1861	CATGTGTTCAATTCTGGCAATGAAGTGATATTGAACCGTATGTGATTTGTGCTTCGGA	1920
Db	1861	CATGTGTTCAATTCTGGCAATGAAGTGATATTGAACCGTATGTGATTTGTGCTTCGGA	1920
QY	1921	GTTACTCTTCGAGCGTGAATTCATGCTGAAGTTTGTATGATGATAGGATGAAGATTTCCACA	2040
Db	1921	GTTACTCTTCGAGCGTGAATTCATGCTGAAGTTTGTATGATGATAGGATGAAGATTTCCACA	2040
QY	1981	TAGTCCGTATCGTAGTGAAATGGTCTATGTGTGATGATTAGGATGAAGATTTCCACA	2040

Db	1981	TAGTGCCTATCTAGTACGTGCGAAATGCTCTATGCTGTGATGTTAGGGATGGAAGATTCCACA	2040
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Db	2041	ACGGAAACGCATATACAGTTGTGGCCATGCAAGTCTAAATACAGATGCAAAATCAGCTTGGGA	2100
Qy	2101	CTTTGAAAGAGACAAATACATTAATCTATGCAATGTAAGAAAGTGTTTAACTTAATCTTAAGGGTACA	2160
Db	2101	CTTTGAAAGAGACAAATACATTAATCTATGCAATGTAAGAAAGTGTTTAACTTAATCTTAAGGGTACA	2160
Qy	2161	GTCCGGAGTCTATATGATGATCTATATGATTCATATGTCGCAATACCTGCTGCAACGATGCCACCGCT	2220
Db	2161	GTCCGGAGTCTATATGATGATCTATATGATTCATATGTCGCAATACCTGCTGCAACGATGCCACCGCT	2220
Qy	2221	GGCAAAATATGGGATATATGGAACCATCATTAATTCACAGATCTAAGTCTAAGTTTATACAGCGA	2280
Db	2221	GGCAAAATATGGGATATATGGAACCATCATTAATTCACAGATCTAAGTCTAAGTTTATACAGCGA	2280
Qy	2281	CATCAGGGAAACAGTGTATACCACTTACGGGCAAAACCAATTTAATGCGTTAGTCAAG	2340
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Db	2461	AACAAACAGTGGGCTCTTTATATGACAGATGTTCAATACGTCCTCAGCAAAACCGAATATATT	2520
Qy	2521	GCCTTAACAGATATCTTAATATATACGGGAAACAGTTTGTAAAGATCTCTCTTGTGGCCTG	2580
Db	2521	GCCTTAACAGATATCTTAATATATACGGGAAACAGTTTGTAAAGATCTCTCTTGTGGCCTG	2580
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Db	2701	TCCATGTGGACCCCAAAACCAATATATGTTTACCAATATTTTGTATPAGACGATTAACAAAGCTTG	2760
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ACCESSION	AX044391		
VERSION	AX044391.1		
KEYWORDS	AX044391.1 GI:11343269		
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Christou, P. and Mehio, L.		
TITLE	Peptideal fusions		
JOURNAL	Patent: WO 006755-A 7 09-NOV-2000;		
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Best Local Similarity	100.0%	Pred. NO. 0		
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			Indels	0
			Gaps	0
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Dd	1	AAATAGATTCTGTTTCGTAAACAGTTTTGTATAAATAAAAACTATAAATATCCG	60	
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Dd	61	GATTATTATACCCTGCCCAACCATGGGGCGCGATTCATAGACAAACCCAAACATCAAC	120	
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Dd	241	GAGTTCGCGCAGAGGCTGGGTGGTGGTCCGCACTAAGTTGACATATCTGGGGTATCTTT	300	
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Dd	301	GGTCCATCTCAATGGGATGATCTCTCGGTGCAATTTGACAGTTGATCAACCAAGATC	360	
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Dd	361	GAAGAGTTGGCCAGAACCCAGGCCATCTCTAGTTGGAAAGTTAGCAATCTTACCAA	420	
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Dd	481	GAATGCGTATTCAATTCAACGACATGAAACAGCGCTTGACCAAGCTATCCCATTTTC	540	
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Dd	601	CTCAGCGTGTTCGAGACGTTAGCGTGTGTTGGGCAAAAGTGGGATTCGATGCTGCAC	660	
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Dd	781	TACAACCAAGTTCCAGAGAGATTTGACCTTCACAGTTTGGACATTTGTCTCTTCCCG	840	
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Dd	841	AACATGACTCCAGAACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT	900	
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Dd	901	ACTAACCAAGTTCTTGAAGCTTGCAGCGTAGCTTCCGTGTTCTGCCCAGGATTCGA	960	

Db 901 ACTAACCAATTCTTGAGAACTTGACGGTAGCTTCGGTGGTCTGCCCAAGATTCGAA 960

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Qy 2041 ACGGAAGCAATACAGTTGTGGCATGCAAGTCTAATACAGATGCAATACAGTCTTGA 2100

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Qy 2161 GTCCGGAAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220

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Qy 2221 GGCATAATATGGAATATGGAACCATCAATTAATCCAGATCTAGTCTAGTTTACAGCA 2280

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Db 2341 GTTGCTTCTCTACTAATATATACACACTTTTGTACAAACATTTGGGCTATATGATC 2400

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Qy 2461 AACAAAGTGGGCTTTTATGACAGATGATGATGATGATGATGATGATGATGATGATGAT 2520

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Qy 2521 GCCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580

Db 2521 GCCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580

Qy 2581 CATCCTTGGGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640

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RESULT 3

AX044392

LOCUS AX044392 2436 bp DNA linear PAT 24-NOV-2000

DEFINITION Sequence 8 from Patent WO0066755.

ACCESSION AX044392

VERSION AX044392.1 GI:11343270

KEYWORDS

SOURCE

ORGANISM

synthetic construct

artificial sequences.

REFERENCE

1 Christou, P. and Menlo, L.

AUTHORS

TITLE

Patent: WO 0066755-A 8 09-NOV-2000;

JOURNAL

Plant Bioscience Limited (GB)

FEATURES

source

1. 2436

/organism="synthetic construct"

/mol type="genomic DNA"

/db xref="taxon:32630"

/note="nucleotide sequence of CryIa(b)-RmB3 in pFASTBAC1"

BASE COUNT 654 a 617 c 521 g 644 t

ORIGIN

Query Match 86.4%; Score 2407.6; DB 6; Length 2436;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2416; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy	1	AAATPAGATATTTTACGTGTTTTGCGTAACAGTTTTGGTATATAAAAAACCTATPAAATATTTCCG	60
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Qy	61	GATTATTTCAATACCGTCCACCACATCGGGCGGGATTCATGAGCAACAACCCAAATCATCAAC	120
Dp	61	GATTATTTCAATACCGTCCACCACATCGGGCGGGATTCATGAGCAACAACCCAAATCATCAAC	120
Qy	121	GAATGCATTTCCATTCGAACCTGCTTGAATPACCCAGAACTTGAAGTACTTGGTGGAAACGC	180
Dp	121	GAATGCATTTCCATTCGAACCTGCTTGAATPACCCAGAACTTGAAGTACTTGGTGGAAACGC	180
Qy	181	ATTGAAACCGGGTACATCTCCCATGAGATCTCCCTGTGCTTGACACAGTTTTCGCTCAGC	240
Dp	181	ATTGAAACCGGGTACATCTCCCATGAGATCTCCCTGTGCTTGACACAGTTTTCGCTCAGC	240
Qy	241	GAGTTGCTGCGCAGGTGCTGGGTTGCTTCTCGGACTAGTTGACATCATTTGGGGTATCTTT	300
Dp	241	GAGTTGCTGCGCAGGTGCTGGGTTGCTTCTCGGACTAGTTGACATCATTTGGGGTATCTTT	300
Qy	301	GGTCCATCTCAATGGGATGCAATTCCTGCTGCAAAATGACAGTTGATCAACGAGGATC	360
Dp	301	GGTCCATCTCAATGGGATGCAATTCCTGCTGCAAAATGACAGTTGATCAACGAGGATC	360
Qy	361	GAAGAGTTCCGCGAGGAACCAAGGCGCATCTTAGTTGGAAAGGATTTGACAAATCTCTACAA	420
Dp	361	GAAGAGTTCCGCGAGGAACCAAGGCGCATCTTAGTTGGAAAGGATTTGACAAATCTCTACAA	420
Qy	421	ATCTATGACAGAGCTTCAGAGAGTGGAAAGCCGATCTCTACTAACCCAGCTCTCCGAG	480
Dp	421	ATCTATGACAGAGCTTCAGAGAGTGGAAAGCCGATCTCTACTAACCCAGCTCTCCGAG	480
Qy	481	GAATTGGGTATTAATTTCAACGATGAACAAGGCGCTTGACCAAGCATTCCTCATTTCTTC	540
Dp	481	GAATTGGGTATTAATTTCAACGATGAACAAGGCGCTTGACCAAGCATTCCTCATTTCTTC	540
Qy	541	GCACTCCAGAACTACCAAGTTCCCTCTCTTGCTCGGTACGTTCAAGCAGCTAAATCTTCAC	600
Dp	541	GCACTCCAGAACTACCAAGTTCCCTCTCTTGCTCGGTACGTTCAAGCAGCTAAATCTTCAC	600
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Dp	721	CGTTGGTACAACTGTGCTTGGAGCGTGTCTGGGGTCTCTGATTTCTAAGATTGGATTAGA	780
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Dp	781	TACAACAGGTTCAGAGAGAAATPACCTCACAAGTTTGGACATTTGTCCTCTTCCG	840
Qy	841	AACATGATCTCCAGAACCTTACCTTATCCGTACAGTGTCCCACTTACAGAGAAATCTAT	900
Dp	841	AACATGATCTCCAGAACCTTACCTTATCCGTACAGTGTCCCACTTACAGAGAAATCTAT	900
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Dp	901	ACTAACCCAGTTCTTGAGAACTTGAACGATAGCTTCCGTGGTTCTGCCCCAAGGTATGAA	960
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Dp	961	GGCTTCATCAGAGAGCCACCTTGAATGACATCTTTGAACACATPACTATCAACCGAT	1020
Qy	1021	GCTCACAGAGAGATATTACTGGTCTGGACACACAGATCATGGCCTCTCCAGTTGGATTTC	1080
Dp	1021	GCTCACAGAGAGATATTACTGGTCTGGACACACAGATCATGGCCTCTCCAGTTGGATTTC	1080

QY	1081	AGCGGCCCCGAGTTAACTCTTTCCTCTCTATGGAACATAATGGAAGAGCGCGCTCCAGAACAA	1140
Db	1081	AGCGGCCCCGAGTTAACTCTTTCCTCTCTATGGAACATAATGGAAGAGCGCGCTCCAGAACAA	1140
QY	1141	CGTATCGTGTGCTCAACTAGTCCAGGGGTGTCTACAGAACCTTGTCTTCCACTTGTATCAGA	1200
Db	1141	CGTATCGTGTGCTCAACTAGTCCAGGGGTGTCTACAGAACCTTGTCTTCCACTTGTATCAGA	1200
QY	1201	AGACCTTTCAAATATCGGTATCAACACAGCAACTTTCCGTTCTTGAACGAAACAGAGTTTC	1260
Db	1201	AGACCTTTCAAATATCGGTATCAACACAGCAACTTTCCGTTCTTGAACGAAACAGAGTTTC	1260
QY	1261	GCCTATGGAACTCTTCTTAACCTTGCGCATCCCGGTGTTTACAGAAAGACCGGAACCGTTGAT	1320
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Db	1321	TCCTTTGACGAAATCCACCAACAGAACCAATGTGCCACCCAGGCAGAGATTCTTCCAC	1380
QY	1381	AGGTTGACCCACGTCGTCCATGTTCCGTTCCGGATTCCAGCAACAGTTCCGTGAGCATCATC	1440
Db	1381	AGGTTGACCCACGTCGTCCATGTTCCGTTCCGGATTCCAGCAACAGTTCCGTGAGCATCATC	1440
QY	1441	AGAGCTCCATAGTTCTCATGAGATTTCATCGTAGTGTGATGATTCACAAATATCATTTCTTCC	1500
Db	1441	AGAGCTCCATAGTTCTCATGAGATTTCATCGTAGTGTGATGATTCACAAATATCATTTCTTCC	1500
QY	1501	TCTCAAAATCACCCAAATCCCATTTGACCAAGTCTACTTAACTTGGATCTGTGAACTTGTGC	1560
Db	1501	TCTCAAAATCACCCAAATCCCATTTGACCAAGTCTACTTAACTTGGATCTGTGAACTTGTGC	1560
QY	1561	GTGAAGAAGACCAAGGCTTCCACAGAGAGTATATTCTTGAAGAACTTCTCTGGCCAGATT	1620
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QY	1621	AGACCCCTCAGAGTTAACATCATCTGCACCACTTTCTCAAGAATATCGTGCAGAGATTTCGT	1680
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Db	1681	TACGATATCAACACTTAACCTTGCAATTTCCACACCTCCATGAGGAAGGCTATCATTCAG	1740
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QY	1921	GTTACCTTTCGAGGCGTAGTACTGAGAAATTCATGCTGATGTTTGTATGATCCTGACGCCA	1980
Db	1921	GTTACCTTTCGAGGCGTAGTACTGAGAAATTCATGCTGATGTTTGTATGATCCTGACGCCA	1980
QY	1981	TAGTCGATCGTAGGTCGAAATGCGTATGTGTGATGATGTTAGGAGATGGAAGATTCCACA	2040
Db	1981	TAGTCGATCGTAGGTCGAAATGCGTATGTGTGATGATGTTAGGAGATGGAAGATTCCACA	2040
QY	2041	ACGGAACCGCAATACAGTTGTGGCCCATGCAAGTCTTAATACAGATGCAAAATCAGCTTGGAA	2100
Db	2041	ACGGAACCGCAATACAGTTGTGGCCCATGCAAGTCTTAATACAGATGCAAAATCAGCTTGGAA	2100
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Db	2101	CTTTGAAAAGACAAATCTATTTGATCTCTAATGGAAGAGGTTTAACTACTTACGGGTACA	2160
QY	2161	GTCGGGAGTCTATGTGATGATCTATGATTGGCAATACCTGCTGCACACTGATCCACCCT	2220

Db	2161	GTCCGGAGCTTAATGTGATGATCTTAATGATTCGAAATCTGCTGCACTGATGCCACCGCT	2220
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Db	2221	GGCAAAATATGGATTAATGGAACCAATCAATAAATCCAGATCTAGTCTAGTTTATGACAGGA	2280
Qy	2281	CATCAGGGAACAGTGTGTCCACACTTTCAGGTGCAACCAACATTTATGCGGTATGTCAG	2340
Db	2281	CATCAGGGAACAGTGTGTCCACACTTTCAGGTGCAACCAACATTTATGCGGTATGTCAG	2340
Qy	2341	GTGCGCTTCCACTAATAATACACACCTTTTGTATCAACACCATTTGGTGGGTATATGCTC	2400
Db	2341	GTGCGCTTCCACTAATAATACACACCTTTTGTATCAACACCATTTGGTGGGTATATGCTC	2400
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VERSION	AX044393.1	GI:11343271	
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	1		
TITLE	Christou, P. and Mehlo, L.		
JOURNAL	Pesticidal fusions		
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Best Local Similarity:	90.7%;	Pred. No. 0;	
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Qy	61	GATTATTCATACCGGCCACCAATGGGGGGGATTCATGAGCAACAACCAACATCAAC	120
Db	61	GATTATTCATACCGGCCACCAATGGGGGGGATTCATGAGCAACAACCAACATCAAC	120
Qy	121	GAATGATTCATCACTACCACTGCTGTGAGTAAACGAGAAGTTGAAGTCTTGAGAGAGCG	180
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Qy	241	GAGTTCGTGACAGGCTGGGTTGGTCTCCGCACTAGTTGACATCATCGGGGTATCTTT	300
Db	241	GAGTTCGTGACAGGCTGGGTTGGTCTCCGCACTAGTTGACATCATCGGGGTATCTTT	300
Qy	301	GGTCCATCTCAATGGGATGTCATCTCGTGTGCAAAATTGACAGTTGATCAACAGAGATC	360
Db	301	GGTCCATCTCAATGGGATGTCATCTCGTGTGCAAAATTGACAGTTGATCAACAGAGATC	360
Qy	361	GAAAGATTGCCAGAACCCAGGCATCTTCTAGGTTGAAAGATTGAGCAATCTTACCA	420

Dp	361	GAAGAGTTCCGCCAGAAACAGGCCATTCTTAGTGTGGAGAGATTGAGCAATCTCTACCA	420
Qy	421	ATCTATGCAAGAGCTTCAGAGATGGGAAGCCGATCTTACTAACCCAGCTCTCCGAG	480
Dp	421	ATCTATGCAAGAGCTTCAGAGATGGGAAGCCGATCTCTAACCCAGCTCTCCGAG	480
Qy	481	GAATGGGTATTCAATTCACGACATGAAACAGGCCCTTGACACAGCTATCCCATTTGTC	540
Dp	481	GAATGGGTATTCAATTCACGACATGAAACAGGCCCTTGACACAGCTATCCCATTTGTC	540
Qy	541	GCAGTCCAGAACTACCAAGTTCCCTCTTGTCCGTGACCTTAAGCAGCTTAATCTTCAC	600
Dp	541	GCAGTCCAGAACTACCAAGTTCCCTCTTGTCCGTGACCTTAAGCAGCTTAATCTTCAC	600
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Dp	661	ATCAATATGCCGTTTCAACGACCTTACTAGCTGATTTGGAAACTACACCCGACACGCTGTT	720
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Dp	721	CGTTGGTACAACTGAGCTTGGAGCGGTCTGGGGGTCTGATTTCTAGATTGGAATTAGA	780
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Dp	781	TACAACCAAGTTACAGAGAGAAATTGACCCCTCAGATTGTGGACATTTGCTCTCTCCG	840
Qy	841	AACTATGATCTTCAGAACCTTACCTTATCCGTAACAGTGTCCCACTTACCAAGAAATCTAT	900
Dp	841	AACTATGATCTTCAGAACCTTACCTTATCCGTAACAGTGTCCCACTTACCAAGAAATCTAT	900
Qy	901	ACTAATCCAGTCTTGGAACTTGGAGAGTTCGCTGGGTCTGGCCCAAGATATGAA	960
Dp	901	ACTAATCCAGTCTTGGAACTTGGAGAGTTCGCTGGGTCTGGCCCAAGATATGAA	960
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Dp	961	GGCTTCATCAAGAGCCCACTTGATGAGACATCTTGAACAGCATMACTATCTACCCGAT	1020
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Dp	1021	GCTCAACAGAGAGATTTACTGCTTGACACAGATCATGAGCTCTCCAGTTGATTC	1080
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Dp	1201	AGACCTTCAATATCGGTATCAACACACGCACTTTCGTTCTTGACGGAACAGATTC	1260
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Qy	1321	TCCTTGAAGAAATCCCAACAGAACCAATGTGCACCCAGGCAAGATTTCTCCAC	1380
Dp	1321	TCCTTGAAGAAATCCCAACAGAACCAATGTGCACCCAGGCAAGATTTCTCCAC	1380
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Qy	1441	AGAGTCTCATATGTTCTCATGGAATCATGTATGTGATGTTCAACAATATGATTCCTTC	1500
Dp	1441	AGAGTCTCATATGTTCTCATGGAATCATGTATGTGATGTTCAACAATATGATTCCTTC	1500

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RESULT 5
 AX044394
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 VERSION AX044394.1 GI:11343272
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LOCUS Sequence 11 from Patent W0006755.
DEFINITION AX044395
ACCESSION AX044395
VERSION AX044395.1 GI:11343273
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Christou, P. and Mehlo, L.
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Plant Bioscience Limited (GB)
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ORIGIN

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ACCESSION AX044385
VERSION AX044385.1 GI:11343263
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Christou, P. and Mehlo, L.
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RESULT 8
 AR110602
 LOCUS AR110602 7378 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 9 from patent US 6114608.
 ACCESSION AR110602
 VERSION AR110602.1 GI:12826878
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 7378)
 AUTHORS Mettler, I.J., Dietrich, P.S. and Sinibaldi, R.M.
 TITLE Nucleic acid construct comprising bacillus thuringiensis cry1Ab gene
 JOURNAL Patent: US 6114608-A 9 05-SEP-2000;
 FEATURES
 source 1..7378
 location/Qualifiers
 BASE COUNT 1917 a 1803 c 1719 g 1939 t
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 QY 95 CCATTGACAAACCAACCAATCATCAAGATGCAATTCATCACTGCTGAGTAAACCCAG 154
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QY 1955 T 1955
 DB 2880 T 2880
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 LOCUS ARI51001 7378 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 9 from patent US 6229075.
 ACCESSION ARI51001
 VERSION ARI51001.1 GI:15115592
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 7378)
 Mettler, I.J., Plaisted, D.C., Grier, S.L., Houghton, W. and
 AUTHORS Gardiner, M.
 TITLE Indred maize line R412H
 JOURNAL Patent: US 6229075-A 9 08-MAY-2001;
 FEATURES
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 BASE COUNT 1917 a 1803 c 1719 g 1939 t
 ORIGIN
 Query Match 66.3%; Score 1848.2; DB 6; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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 Db 2880 T 2880
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 AR152424 7378 bp DNA linear PAT 08-AUG-2001
 LOCUS AR152424
 DEFINITION Sequence 9 from patent US 6232533.
 ACCESSION AR152424
 VERSION AR152424.1 GI:15118474
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 7378)
 AUTHORS Mettler,I.J., Plaisted,D.C., Griener,S.L., Houghton,W. and Gardiner,M.
 TITLE Inbred maize line R372H
 JOURNAL Patent: US 6232533-A 9 15-MAY-2001;
 FEATURES
 source Location/Qualifiers
 1..7378 /organism="unknown"
 BASE COUNT 1917 a 1803 c 1719 g 1939 t
 ORIGIN
 Query Match 66.3%; Score 1848.2; DB 6; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 95 CCATGGAACAACCAACCAACATCAACGATGATTCATCAACGATGCTTGAAGTAAACCGAG 154
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RESULT 11
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 DEFINITION Sequence 9 from patent US 6232534.
 ACCESSION AR152433
 VERSION AR152433.1 GI:15118483
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 7378)
 AUTHORS Mettler, I. J., Plaisted, D. C., Grier, S. L., Houghton, W. and Gardiner, M.
 TITLE Inbred maize line R660H
 JOURNAL Patent: US 6232534-A 9 15-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..7378
 BASE COUNT 1917 a 1803 c 1719 g 1939 t
 ORIGIN

Query Match 66.3%; Score 1848.2; DB 6; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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 QY 755 GTCTGATTTAGAGATTGATTTGATTTCAACCAAGTTAGAGAGAAATTGACCTCAGC 814
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 Db 1680 GTCTGATTTAGAGATTGATTTGATTTCAACCAAGTTAGAGAGAAATTGACCTCAGC 1739
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 Db 1920 TGAACAGATATCTATCTACACCGAGTCTCACAAGAGAGATTTACTGCTGGAACCC 1979
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 QY 1955 T 1955
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 Db 2880 T 2880
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RESULT 12
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 LOCUS AR184317 7378 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 9 from patent US 6342660.
 ACCESSION AR184317
 VERSION AR184317.1 GI:20228286
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 7378)
 AUTHORS Mettler, J., Plaisted, D.C., Grier, S.L., Houghton, W. and Gardiner, M.
 TITLE DNA construct containing Bacillus thuringiensis gene and plants containing it
 JOURNAL Patent: US 6342660-A 9 29-JAN-2002;
 FEATURES
 source location/Qualifiers
 1..7378
 /organism="unknown"
 BASE COUNT 1917 a 1803 c 1719 g 1939 t
 ORIGIN
 Query Match 66.3%; Score 1848.2; DB 6; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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 Db 1500 TGTAGCTTCAAGCAGCTATCTTCACTCAGCGTCTTCGAGACGTTAGGTTGGGC 1559
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 Db 2100 GAACCTTGTCTTCACCTTGTACAGAAACCTTCAATATCGGTATCAACAACGCAAC 2159
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 Qy 1415 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGG 1474
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 Db 2580 CTCAAGATATCGTGTGAGATTCGTTAGCATTCACCTTACCTTGAATTTCAACCT 2639
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 Qy 1895 ACCGATATGATTTGTGTGCTGCGGAGTTACCTTCGAGGCTGAGTACAGAAATTCATGC 1954
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 Qy 1955 T 1955
 Db 2880 T 2880

RESULT 13
 AR212558 7378 bp DNA linear PAT 20-JUN-2002
 LOCUS AR212558
 DEFINITION Sequence 9 from patent US 6399860.
 ACCESSION AR212558
 VERSION AR212558.1 GI:21516165
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 7378)
 Mettler, I. J., Plaisted, D. C., Grier, S. L., Houghton, W. and
 Gardiner, M.
 TITLE Inbred maize line R327H
 JOURNAL Patent: US 6399860-A 9 04-JUN-2002;
 FEATURES
 source 1..7378
 BASE COUNT 1917 a 1803 c 1719 g 1939 t
 ORIGIN

Query Match 66.3%; Score 1848.2; DB 6; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 95 CCATGAGCAACAACCAACATCAACGATTCATACAACTGCTTGAATCAACCGAG 154
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Qy 1955 T 1955
Dh 2880 T 2880

RESULT 14
LOCUS AR110596 1851 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6114608.
ACCESSION AR110596
VERSION AR110596.1 GI:12826872
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1851)
AUTHORS Mettler,I.J., Dietrich,P.S. and Sinibaldi,R.M.
TITLE Nucleic acid construct comprising bacillus thuringiensis cryIab gene
JOURNAL Patent: US 6114608-A 3 05-SEP-2000;
FEATURES
source Location/Qualifiers
BASE COUNT 478 a 504 c 394 g 475 t
ORIGIN
Query Match 66.2%; Score 1845.4; DB 6; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 1801 CCGTATGAGTTTGTGCTGCGGAGATTAATCTTGAAGGCTGAGTACT 1847

RESULT 15
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 LOCUS ARI50995 Sequence 3 from parent US 6229075.
 DEFINITION ARI50995
 ACCESSION ARI50995
 VERSION ARI50995.1 GI:15115586
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 1851)
 Mettler, J., Plaisted, D.C., Grier, S.L., Houghton, W. and
 Gardner, M.
 TITLE
 JOURNAL
 Patent: US 6229075-A 3 08-MAY-2001;
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 Best local Similarity 99.9%; Pred. No. 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 21, 2003, 05:00:28 ; Search time 706 Seconds

(without alignments)
10660.104 Million cell updates/sec

Title: US-09-980-650-6

Perfect score: 2788
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Gapop 10%0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2788	100.0	2788	22	AAA88919
2	2659.4	95.4	2692	22	AAA88920
3	2407.6	86.4	2436	22	AAA88921
4	2333.2	83.7	2788	22	AAA88922
5	2204.6	79.1	2692	22	AAA88923
6	1952.8	70.0	2436	22	AAA88924
7	1951	70.0	2062	22	AAA88914
8	1848.2	66.3	7378	21	AAA75466

9	1848.2	66.3	7378	22	AA06314	Plasmid pZ01502 co
10	1848.2	66.3	7378	22	AA06368	Plasmid pZ01502 co
11	1848.2	66.3	7378	22	AA89825	Nucleotide sequenc
12	1848.2	66.3	7378	22	AA89834	Nucleotide sequenc
13	1848.2	66.3	7378	24	AB157440	Plasmid pZ01502 en
14	1845.4	66.2	1851	21	AAA75460	Nucleotide sequenc
15	1845.4	66.2	1851	22	AA06308	Insecticidal CryIA
16	1845.4	66.2	1851	22	AA06332	Insecticidal CryIA
17	1845.4	66.2	1851	22	AA89819	Nucleotide sequenc
18	1845.4	66.2	1851	22	AA89828	Nucleotide sequenc
19	1845.4	66.2	1851	24	AB157443	CryIab crystal pro
20	1845	66.2	1845	11	AA05792	Encodes modified B
21	1845	66.2	1845	20	AA231666	Artificially modif
22	1844.8	66.2	3484	19	AAV00355	Insecticidal gene
23	1844.8	66.2	3484	22	AA873311	Modified Bacillus
24	1843.8	66.1	1851	22	AA06373	CryIab toxin DNA o
25	1843.4	66.1	3531	19	AAV00293	Bacillus thuringie
26	1843.4	66.1	3531	22	AA873209	Modified Bacillus
27	1838.6	65.9	3531	22	AA808961	B.t.k. HD-73/HD-1
28	1837	65.9	1845	22	AA808947	Bacillus thuringie
29	1507.8	54.1	2062	22	AA88915	Nucleotide sequenc
30	1416.2	50.8	1962	21	AA259084	B. thuringiensis C
31	1411.8	50.6	1920	11	AA005793	Encodes modified B
32	1411.8	50.6	1920	22	AA808955	Bacillus thuringie
33	1411.8	50.6	3534	11	AA005794	Encodes modified B
34	1411.8	50.6	3534	11	AA005795	Encodes full-length
35	1411.8	50.6	3534	11	AA006561	Encodes full-length
36	1411.8	50.6	3534	22	AA808957	Bacillus thuringie
37	1411.8	50.6	3534	22	AA808960	B.t.k. fully synth
38	1407	50.5	3534	22	AA808959	B.t.k. synthetic f
39	1392.6	49.9	3478	19	AAV00291	Insecticidal prote
40	1392.6	49.9	3478	22	AA873207	Modified Bacillus
41	1328.8	47.7	1767	22	AA808953	Bacillus thuringie
42	1325.6	47.5	1767	11	AA005791	Encodes modified B
43	1222	43.8	4360	10	AA850934	Chimeric gene codi
44	1220.4	43.8	2815	11	AA004024	Gene pM2 encoding
45	1220.4	43.8	3066	11	AA004025	Gene pM2 encoding

ALIGNMENTS

RESULT 1	
AAA88919	standard; DNA; 2788 BP.
ID	AAA88919
XX	AAA88919;
AC	
XX	
DT	05-MAR-2001 (first entry)
XX	
DE	Nucleotide sequence of CryIA(b)-RTB1 fusion in pFASTBAC1.
XX	
XX	CryIA(b); crystal protein; ricin toxin B; RTB1; lectin;
KW	insecticide; pesticide; toxin; transgenic plant; insect resistance;
KW	crop protection; pFASTBAC1; ds.
XX	
XX	Chimeric - Bacillus thuringiensis.
OS	Chimeric - Ricinus communis.
OS	Chimeric - Baculovirus.
XX	
XX	WO200066755-A2.
XX	
XX	09-NOV-2000.
PD	
XX	
PF	27-APR-2000; 2000WO-GB01633.
XX	
PR	28-APR-1999; 99GB-0009796.
XX	
PA	(PLAN-) PLANT BIOSCIENCE LTD.
XX	
PI	Christou P, Menlo L;
XX	
DR	WPI; 2001-007228/01.

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Db	2281	CATCAGGGAACAGTGTATCCACAACCTTACGGTGCAAAACCAACATTTATGCGTTAGTCAAG	2340
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RESULT 2
AAA8920
ID AAA8920 standard; DNA; 2692 BP.
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AC AAA8920;
XX
DT 05-MAR-2001 (first entry)
XX
Nucleotide sequence of CRYIA(b) -RTB fusion in pFASTBAC1.
DE
XX CRYIA(b); crystal protein; ricin toxin B; RTB2; lectin;
XX insecticide; pesticide; toxin; transgenic plant; insect resistance;
KW crop protection; pFASTBAC1; ds.
XX
OS Chimeric - Bacillus thuringiensis.
OS Chimeric - Ricinus communis.
OS Chimeric - Baculovirus.
XX
PN WO20006755-A2.
XX
PD 09-NOV-2000.
XX
PF 27-APR-2000; 2000WO-GB01633.
XX
PR 28-APR-1999; 99GB-0009796.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Christou P, Mehlo L;
DR WPI; 2001-007228/O1.
XX
PT Novel nucleic acid molecule encoding a pesticidal fusion polypeptide
PT comprising a toxin and a binding domain for producing transgenic plants
PT resistant to pests -
XX
PS Claim 11; Fig 3g; 81pp; English.
XX
CC This nucleotide sequence is that of a fusion between DNA encoding
CC crystal protein CRYIA(b) (see AAA88914) of <i>Bacillus thuringiensis</i> and
CC DNA encoding ricin toxin B RTB2 (see AAA8917) in baculovirus transfer
CC vector pFASTBAC1, in which the fusion was cloned under the control
CC of the polyhedrin promoter. This is an example of claimed nucleic
CC acids encoding pesticidal fusion proteins between a toxin domain
CC and a heterologous binding domain capable of binding non-specifically
CC to a cell membrane without disrupting that membrane. The use of such
CC fusions may help to inhibit the acquisition of resistance in a pest
CC population treated with the protein. Vectors (e.g. baculovirus
CC vectors or vectors suitable for use in a plant), host cells, and
CC transgenic plants (especially rice or maize) are also provided.
CC Expression of the fusion protein in a plant is useful for influencing
CC or affecting the toxicity of a plant to a pest, allowing control of
CC e.g. Lepidoptera, Coleoptera, Culicidae, Stimuliidae, Hymenoptera,
CC Homoptera, Diptera and Orthoptera pests.
XX
SQ Sequence 2692 BP; 730 A; 660 C; 586 G; 716 T; 0 other;
Query Match 95.4%; Score 2659.4; DB 22; Length 2692;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2660; Conservative 0; Mismatches 1; Indels 0; Gaps 0
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DB 61 GATTATTCATACCGTCCCAACCATGGGCGCGGATGCATGACACAAACCCAAACATCMAAC 120
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Db 2041 ACGGAAACGCAATACAGTTGTGCGCATGCAAGTCTTAATACAGATGCAATCAGCTTGA 2100
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QY 2101 CTTTGAAGAAGACAAATATTTGATCTTAATGGAAGTGTTAATCTTAATCGGGTACA 2160
| | | | |
Db 2101 CTTTGAAGAAGACAAATATTTGATCTTAATGGAAGTGTGTAACTTAATCGGGTACA 2160
| | | | |
QY 2161 GTCCGGAGTGTATGTATGTATGATATGCAATACCTGCAACCTGATGCAACCGCT 2220
| | | | |
Db 2161 GTCCGGAGTGTATGTATGTATGATATGCAATACCTGCAACCTGATGCAACCGCT 2220
| | | | |
QY 2221 GGCATAATATGGGATATGGAACCATATCAATATCCAGATCTAGTCTGATTAGACAGGA 2280
| | | | |
Db 2221 GGCATAATATGGGATATGGAACCATATCAATATCCAGATCTAGTCTGATTAGACAGGA 2280
| | | | |
QY 2281 CATCAGGAAACAGTGTATCACTTACAGTGTGCAACCAATTTATGCGGTATGTCAG 2340
| | | | |
Db 2281 CATCAGGAAACAGTGTATCACTTACAGTGTGCAACCAATTTATGCGGTATGTCAG 2340
| | | | |
QY 2341 GTTGGCTTCTTACTAATATATACAACTTTGTTACAAACATGTTGGGCTATATGGTC 2400
| | | | |

Db 2241 GTTGCTTCTACTAATATACACACCTTTTGTACACCATTTGGCTATATGTC 2400
Qy 2401 TGTGCTTGCAGCAAAATAGTGGACAGATGATGAGAGACTGTAGCAAGTGAAGGCTG 2460
Db 2401 TGTGCTTGCAGCAAAATAGTGGACAGATGATGAGAGACTGTAGCAAGTGAAGGCTG 2460
Qy 2461 AACACAGTGGGCTCTTTATGACAGATGTTCAATACGTCCTCAGCAAAACCGAGATATT 2520
Db 2461 AACACAGTGGGCTCTTTATGACAGATGTTCAATACGTCCTCAGCAAAACCGAGATATT 2520
Qy 2521 GCCTTACAGATGATTTCTAATATACGGGAAACAGTTTAAATCTCTGTGGCCCTG 2580
Db 2521 GCCTTACAGATGATTTCTAATATACGGGAAACAGTTTAAATCTCTGTGGCCCTG 2580
Qy 2581 CATCCTTGCCCAAGATGATGTTCAAGATGATGAAACCATTTAAATTTGTAATGTG 2640
Db 2581 CATCCTTGCCCAAGATGATGTTCAAGATGATGAAACCATTTAAATTTGTAATGTG 2640
Qy 2641 GATTGGTGTATGATGTGAGGC 2661
Db 2641 GATTGGTGTATGATGTGAGGC 2661

RESULT 3
AAA88921
ID AAA88921 standard; DNA; 2436 BP.
XX
AC AAA88921;
XX
DT 05-MAR-2001 (first entry)
XX
DE Nucleotide sequence of CryIA(b)-RTB3 fusion in pFASTBAC1.
XX
KW CryIA(b); crystal protein; ricin toxin B; RTB3; lectin;
KM insecticide; pesticide; toxin; transgenic plant; insect resistance;
XX crop protection; pFASTBAC1; de.
XX
OS Chimeric - *Bacillus thuringiensis*.
OS Chimeric - *Ricinus communis*.
OS Chimeric - *Baculovirus*.
XX
PN WO20006755-A2.
XX
PD 09-NOV-2000.
XX
PE 27-APR-2000; 2000WO-GB01633.
XX
PR 28-APR-1999; 99GB-0009796.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Christou P, Mehio L;
XX
DR WPI; 2001-007228/01.
XX
PT Novel nucleic acid molecule encoding a pesticidal fusion polypeptide
PT comprising a toxin and a binding domain for producing transgenic plants
PT resistant to pests -
XX
PS Claim 11; Fig 3h; 81pp; English.
XX
CC This nucleotide sequence is that of a fusion between DNA encoding
CC crystal protein CryIA(b) (see AAA88914) of *Bacillus thuringiensis* and
CC DNA encoding ricin toxin B RTB3 (see AAA88918) in *Baculovirus* transfer
CC vector pFASTBAC1, in which the fusion was cloned under the control
CC of the polyhedrin promoter. This is an example of claimed nucleic
CC acids encoding pesticidal fusion proteins between a toxin domain
CC and a heterologous binding domain capable of binding non-specifically
CC to a cell membrane without disrupting that membrane. The use of such
CC fusions may help to inhibit the acquisition of resistance in a pest
CC population treated with the protein. Vectors (e.g. *Baculovirus*
CC vectors or vectors suitable for use in a plant) host cells, and
CC transgenic plants (especially rice or maize) are also provided.

CC Expression of the fusion protein in a plant is useful for influencing
CC or affecting the toxicity of a plant to a pest, allowing control of
CC e.g. Lepidoptera, Coleoptera, Culicidae, Hymenoptera,
CC Homoptera, Diptera and Orthoptera pests.
XX
SQ Sequence 2436 BP; 654 A; 617 C; 521 G; 644 T; 0 other;
Query Match 86.4%; Score 2407.6; DB 22; Length 2436;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2416; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 AAATAGTATTTTACCTGTTTTCGTAACAGTTTGTATTAATAAAACCTATTAATTCG 60
Db 1 AAATAGTATTTTACCTGTTTTCGTAACAGTTTGTATTAATAAAACCTATTAATTCG 60
Qy 61 GATTATTCATACCGTCCCAACCATCGGCGCGGATCCATGAGCAACAACCCAAACATCAAC 120
Db 61 GATTATTCATACCGTCCCAACCATCGGCGCGGATCCATGAGCAACAACCCAAACATCAAC 120
Qy 121 GAATGCAATTCATACCACTGCTTGTAGTAACCCAGAAAGTTGAAGTACTTGTGAGAACGC 180
Db 121 GAATGCAATTCATACCACTGCTTGTAGTAACCCAGAAAGTTGAAGTACTTGTGAGAACGC 180
Qy 181 ATTGAACCGGTTACCTCCCATGACATCTCTTCTTGACACAGTTTCTGCTCAGC 240
Db 181 ATTGAACCGGTTACCTCCCATGACATCTCTTCTTGACACAGTTTCTGCTCAGC 240
Qy 241 GAGTTGCGCCAGAGTGCTGGGTTGTTCTCGGATGATGATGATGATGATGATGATGATG 300
Db 241 GAGTTGCGCCAGAGTGCTGGGTTGTTCTCGGATGATGATGATGATGATGATGATGATG 300
Qy 301 GGTCCATCTCAATGGAGATGATTCCTGCGCAATTTGACAGTTGATCAACCAAGATC 360
Db 301 GGTCCATCTCAATGGAGATGATTCCTGCGCAATTTGACAGTTGATCAACCAAGATC 360
Qy 361 GAAAGTTCCGCAAGAACCCAGGCGCATCTTGAAGTTGAAAGATGAGCAATCTTACCAA 420
Db 361 GAAAGTTCCGCAAGAACCCAGGCGCATCTTGAAGTTGAAAGATGAGCAATCTTACCAA 420
Qy 421 ATCTATGAGAGAGCTTCAGAGAGTGGAGCCGATCCTAATACCCAGCTCTCGCAG 480
Db 421 ATCTATGAGAGAGCTTCAGAGAGTGGAGCCGATCCTAATACCCAGCTCTCGCAG 480
Qy 481 GAAATGGGTATTCATTTCAATTCACGATGAACGCGCTTGACCAAGCTATCCATTGTC 540
Db 481 GAAATGGGTATTCATTTCAATTCACGATGAACGCGCTTGACCAAGCTATCCATTGTC 540
Qy 541 GCAATCCAGAACTACCAAGTCTCTCTTTCGCTGATCCTTCAAGCAAGCTATCTTAC 600
Db 541 GCAATCCAGAACTACCAAGTCTCTCTTTCGCTGATCCTTCAAGCAAGCTATCTTAC 600
Qy 601 CTCAGCGTCTTGAAGAGTGGGCTGTTGGGCAAAAGTGGGATTCGATGCTGCAAC 660
Db 601 CTCAGCGTCTTGAAGAGTGGGCTGTTGGGCAAAAGTGGGATTCGATGCTGCAAC 660
Qy 661 ATCAATAGCCGTTTCAACAGACCTTACTAGGCTGATGGAATCTACCCAGCAGCTGTT 720
Db 661 ATCAATAGCCGTTTCAACAGACCTTACTAGGCTGATGGAATCTACCCAGCAGCTGTT 720
Qy 721 CGTTGCTCAACACTGCTGAGCGTGTCTGGGGTCTGATTTCTAGAGATTGATGA 780
Db 721 CGTTGCTCAACACTGCTGAGCGTGTCTGGGGTCTGATTTCTAGAGATTGATGA 780
Qy 781 TACAACAGTTCAGAGAGAAATTGACCTTCAAGTTTGAATGATGATGATGATGATGATG 840
Db 781 TACAACAGTTCAGAGAGAAATTGACCTTCAAGTTTGAATGATGATGATGATGATGATG 840
Qy 841 AACTATGCTCCAGAACTTACCTTATCTGATCAGTGTCCCAATTTACAGAGAAATCTAT 900
Db 841 AACTATGCTCCAGAACTTACCTTATCTGATCAGTGTCCCAATTTACAGAGAAATCTAT 900
Qy 901 ACTAACCGAGTTCTTGAAGACTGCAAGGATGCTTCCGTGTTCTGCAAGATTCGAA 960
Db 901 ACTAACCGAGTTCTTGAAGACTGCAAGGATGCTTCCGTGTTCTGCAAGATTCGAA 960

CC acids encoding pesticidal fusion proteins between a toxin domain
 CC and a heterologous binding domain capable of binding non-specifically
 CC to a cell membrane without disrupting that membrane. The use of such
 CC fusions may help to inhibit the acquisition of resistance in a pest
 CC population treated with the protein. Vectors (e.g. baculovirus
 CC vectors or vectors suitable for use in a plant), host cells, and
 CC transgenic plants (especially rice or maize) are also provided.
 CC Expression of the fusion protein in a plant is useful for influencing
 CC or affecting the toxicity of a plant to a pest, allowing control of
 CC e.g. Lepidoptera, Coleoptera, Culicidae, Simuliidae, Hymenoptera,
 CC Homoptera, Diptera and Orthoptera pests.

XX Sequence 2788 BP; 766 A; 664 C; 607 G; 751 T; 0 other;

Query Match 83.7%; Score 2333.2; DB 22; Length 2788;

Best Local Similarity 90.7%; Pred. No. 0;

Matches 2534; Conservative 0; Mismatches 248; Indels 12; Gaps 4;

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Oy 1 AAATAAGTATTTTACTGTTTTCGTAACAGTTTGTATATPAAAAAACCATAATATTCGG 60
Db 1 AAATAAGTATTTTACTGTTTTCGTAACAGTTTGTATATPAAAAAACCATAATATTCGG 60
Oy 61 GATTATTATACCGTCCCAACCATCGGGCGCGATCCATGAGCAACCAACCAACATCAAC 120
Db 61 GATTATTATACCGTCCCAACCATCGGGCGCGATCCATGAGCAACCAACCAACATCAAC 120
Oy 121 GAATGATTCATACATGCTTGTAGTAACCCAGAAAGTTGAAGTCTTGTTGAGAAAGC 180
Db 121 GAATGATTCATACATGCTTGTAGTAACCCAGAAAGTTGAAGTCTTGTTGAGAAAGC 180
Oy 181 ATTGAACCGGTTTACATCCATCCATGACATCTCTCTGCTTGACACAGTTTCTGCTCAGC 240
Db 181 ATTGAACCGGTTTACATCCATCCATGACATCTCTCTGCTTGACACAGTTTCTGCTCAGC 240
Oy 241 GAGTTCGTCGCGAGTCTGGGTTCTGCTCGGACATGTTGACATATCTGGGGTATCTT 300
Db 241 GAGTTCGTCGCGAGTCTGGGTTCTGCTCGGACATGTTGACATATCTGGGGTATCTT 300
Oy 301 GGTCCATCTCAATGGGATGATCTCTGTCGTAATTTGAGCAGTTGATCAACAGAGATC 360
Db 301 GGTCCATCTCAATGGGATGATCTCTGTCGTAATTTGAGCAGTTGATCAACAGAGATC 360
Oy 361 GAAAGTTCGCGAGAACCCAGGCCATCTTAGTTGGAAGATTGAGCAATCTTCAACAA 420
Db 361 GAAAGTTCGCGAGAACCCAGGCCATCTTAGTTGGAAGATTGAGCAATCTTCAACAA 420
Oy 421 ATCTATGACAGAGCTTCAGAGTGGGAAGCCGATCTTAACCCAGCTCTCCGCGAG 480
Db 421 ATCTATGACAGAGCTTCAGAGTGGGAAGCCGATCTTAACCCAGCTCTCTCCGCGAG 480
Oy 481 GAAATGCGTATTCATATTCAGACATGAACAGCGCTTGACACAGCTATCCCATTTGTC 540
Db 481 GAAATGCGTATTCATATTCAGACATGAACAGCGCTTGACACAGCTATCCCATTTGTC 540
Oy 541 GCAAGTCCAGAACTACCAAGTCTCTCTGTCGCTGATCAGTTCAAGCAGCTATATCTTCA 600
Db 541 GCAAGTCCAGAACTACCAAGTCTCTCTGTCGCTGATCAGTTCAAGCAGCTATATCTTCA 600
Oy 601 CTCACGTCGCTTCGAGACGTTAGCGTTTGGCAAAAGTGGGATTCAGATGTGCAAC 660
Db 601 CTCACGTCGCTTCGAGACGTTAGCGTTTGGCAAAAGTGGGATTCAGATGTGCAAC 660
Oy 661 ATCAATAGCCGTTTACCAAGACCTTACTAGGCTGATTTGAAAATCAACACGACGCTGTT 720
Db 661 ATCAATAGCCGTTTACCAAGACCTTACTAGGCTGATTTGAAAATCAACACGACGCTGTT 720
Oy 721 CGTTGGTATCAACTGCTGGTGAAGCGTGTCTGGGGTCTGATTTCTGAAGATTGGAATTA 780
Db 721 CGTTGGTATCAACTGCTGGTGAAGCGTGTCTGGGGTCTGATTTCTGAAGATTGGAATTA 780
Oy 781 TACAACCAAGTTCGAGAGAAATGACCTCAGAGTTTGGACATGTTGCTCTCTTCCCG 840
Db 781 TACAACCAAGTTCGAGAGAAATGACCTCAGAGTTTGGACATGTTGCTCTCTTCCCG 840

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Oy 841 AACTATGATCTCCAGAACCTTATCCCTATCCGTAAGTGTCCCACTTACCAGAAATCTAT 900
Db 841 AACTATGATCTCCAGAACCTTATCCCTATCCGTAAGTGTCCCACTTACCAGAAATCTAT 900
Oy 901 ACTAATCCAGTCTTGGAAGTTCGAGGATGCTCCGTGGTTCGGCCAAAGTATGAA 960
Db 901 ACTAATCCAGTCTTGGAAGTTCGAGGATGCTCCGTGGTTCGGCCAAAGTATGAA 960
Oy 961 GGCTTCATCAAGAGACCCACACTTGTATGACATCTTTGAACAGCATATATCTACACCAT 1020
Db 961 GGCTTCATCAAGAGACCCACACTTGTATGACATCTTTGAACAGCATATATCTACACCAT 1020
Oy 1021 GCTCAGAGAGAGATATTAATCTGCTGAGACACAGATCATGCTCTCCAGTTGATTC 1080
Db 1021 GCTCAGAGAGAGATATTAATCTGCTGAGACACAGATCATGCTCTCCAGTTGATTC 1080
Oy 1081 AGCGGGCCCGAGTTTACCTTCTCTCTATGGAAGTATGGGAAAGCGCGCTCCACAACAA 1140
Db 1081 AGCGGGCCCGAGTTTACCTTCTCTCTATGGAAGTATGGGAAAGCGCGCTCCACAACAA 1140
Oy 1141 CGTATCGTTCCTCAATAGTCAAGGATGTCAGAGAACTTGTCTCCACCTTGTACAGA 1200
Db 1141 CGTATCGTTCCTCAATAGTCAAGGATGTCAGAGAACTTGTCTCCACCTTGTACAGA 1200
Oy 1201 AGACCTTCAATATCGGTATCAACAACAGCACTTTCGTTCTTGACGAAACAGATTTC 1260
Db 1201 AGACCTTCAATATCGGTATCAACAACAGCACTTTCGTTCTTGACGAAACAGATTTC 1260
Oy 1261 GCTATGGAACCTTCTTCAATTCGTCATCCGCTGTTTACAAAGAGGGAACGTTGAT 1320
Db 1261 GCTATGGAACCTTCTTCAATTCGTCATCCGCTGTTTACAAAGAGGGAACGTTGAT 1320
Oy 1321 TCTTTGACGAATATCCACACAGAAACAATGTGCCACAGGCAAGATTCTCCAC 1380
Db 1321 TCTTTGACGAATATCCACACAGAAACAATGTGCCACAGGCAAGATTCTCCAC 1380
Oy 1381 AGTTGAGCAACAGTGTCCATGCTTCGTTCCGATTCACCAACAGTTCGTCATATC 1440
Db 1381 AGTTGAGCAACAGTGTCCATGCTTCGTTCCGATTCACCAACAGTTCGTCATATC 1440
Oy 1441 AGAGCTCTATGTTCTCATGATTCATGATGCTGATGATCAACATATCATCTTCC 1500
Db 1441 AGAGCTCTATGTTCTCATGATTCATGATGCTGATGATCAACATATCATCTTCC 1500
Oy 1501 TCTCAATACCCCAATCCCATTTGACCAAGTCTTAACTTGAATCTGAACTTCTGTC 1560
Db 1501 TCTCAATACCCCAATCCCATTTGACCAAGTCTTAACTTGAATCTGAACTTCTGTC 1560
Oy 1561 GTGAAAGACCAAGCTTCAACAGAGGATATTTTGAAGAACTTCTCTGCGCAATT 1620
Db 1561 GTGAAAGACCAAGCTTCAACAGAGGATATTTTGAAGAACTTCTCTGCGCAATT 1620
Oy 1621 AGCATCCCTCAGAGTTAATCATCATGTCACCACTT---TCTCAAGATATGTCAGATT 1677
Db 1621 AGCATCCCTCAGAGTTAATCATCATGTCACCACTT---TCTCAAGATATGTCAGATT 1677
Oy 1678 ATTCAGAAATGAGGATATATGAAATTCATATTCATCTCCATCCATCTACAGATAT 1737
Db 1678 ATTCAGAAATGAGGATATATGAAATTCATATTCATCTCCATCCATCTACAGATAT 1737
Oy 1738 CGTTACGATCTACCACTAATCTGCAATTCACACCTCATGACGGAAGGCTTATCAT 1794
Db 1738 CGTTACGATCTACCACTAATCTGCAATTCACACCTCATGACGGAAGGCTTATCAT 1794
Oy 1794 GAGGATATCTTCCGCAACATGTC---AGCGCAGACACTTGCATCCGACGCTTC 1854
Db 1794 GAGGATATCTTCCGCAACATGTC---AGCGCAGACACTTGCATCCGACGCTTC 1854
Oy 1854 AGAAGCGTGGTTCATCTTCACTCTTCAACTCTTCAACGATCAAGCGTTTCAACCTT 1914
Db 1854 AGAAGCGTGGTTCATCTTCACTCTTCAACTCTTCAACGATCAAGCGTTTCAACCTT 1914
Oy 1914 AGCGTCAATGTCATATCTTGGCAATGAAGTATGATGACCGTATGATGATGCTT 1970
Db 1914 AGCGTCAATGTCATATCTTGGCAATGAAGTATGATGACCGTATGATGATGCTT 1970
Oy 1970 GGTGTTAGAACTTTAGTGGAGCTGAGAGATGATATGACAGATTCGAGTTCAATTCGA 1997
Db 1970 GGTGTTAGAACTTTAGTGGAGCTGAGAGATGATATGACAGATTCGAGTTCAATTCGA 1997

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Oy	1915	CCCCAGTTACTCTTCGAGGCGTAGTACGAAATTCATGCGATGTTTGTATGGAATCCTG	1974
Db	1918	GTACTGCAACAACCTCGAGGCTG- --AATGAAATTCACGTGAGTGTGTATGGAATCCTG	1974
Oy	1975	AGCCCATAGTACGATCGTAGTCGAAATGCTCTATGTGTGATGTTAGGATGGAAGAT	2034
Db	1975	AGCCCATAGTACGATCGTAGTCGAAATGCTCTATGTGTGATGTTAGGATGGAAGAT	2034
Oy	2035	TCCACAAACGGAAGCCCAATACAGTTGTGGCCATGCAAGTCTTAATACAGATCCAAATCAGC	2094
Db	2035	TCCAACAACGGAACGCAATACAGTTGTGGCCATGCAAGTCTTAATACAGATCCAAATCAGC	2094
Oy	2095	TCTGGACTTTGAAAAAGAGACAATACTATTCGATCTAAAGGAAAGTGTTAACFTTACG	2154
Db	2095	TCTGGACTTTGAAAAAGAGACAATACTATTCGATCTTAATGAAAGTGTTAATCTATTCAG	2154
Oy	2155	GGTACAGTCGGGAGTCTATGTATGATCTATGATTCGAATACCTGTCGCACTGATGCCA	2214
Db	2155	GGTACAGTCGGGAGTCTATGTATGATCTATGATTCGAATACCTGTCGCACTGATGCCA	2214
Oy	2215	CCCCGTGGCAATAATNGGATTAATGGAACCAATCATTAATCCAGATCTATAGTCTACTTTTAA	2274
Db	2215	CCCCGTGGCAATAATNGGATTAATGGAACCAATCATTAATCCAGATCTATAGTCTACTTTTAA	2274
Oy	2275	CAGCGACATCAGGGAACAGTGGTACCAACACTTACGGTGCAGAACCAACACTTTATGCCCTTA	2334
Db	2275	CAGGACATCAGGGAACAGTGGTACCAACACTTACGGTGCAGAACCAACACTTTATGCCCTTA	2334
Oy	2335	GTCAAGGTGGGCTTCTCTAATAATACACAACCTTTTGTTAACAACCTTGTGGGCTAT	2394
Db	2335	GTCAAGGTGGGCTTCTCTAATAATACACAACCTTTTGTTAACAACCTTGTGGGCTAT	2394
Oy	2395	ATGCTCTGTGCTTCGACAAATATGTGACAAGTATGATAGAGACTGTAGCAGTGA	2454
Db	2395	ATGCTCTGTGCTTCGACAAATATGTGACAAGTATGATAGAGACTGTAGCAGTGA	2454
Oy	2455	AGGCTGAACAACAGTGGGCTCTTATATGCAAGTGTCAATACGTCCTCAGCAAAACCGAG	2514
Db	2455	AGGCTGAACAACAGTGGGCTCTTATATGCAAGTGTCAATACGTCCTCAGCAAAACCGAG	2514
Oy	2515	ATAATTTGCTTACAAGTATCTATATACGGGAAACAGTTTAAGATCCCTCTGTG	2574
Db	2515	ATAATTTGCTTACAAGTATCTATATACGGGAAACAGTTTAAGATCCCTCTGTGTG	2574
Oy	2575	GCCCTGCATCCCTCTGGCCACAGATGATGTTCCAGAAATGATGGAACCAATTTTAATTTGT	2634
Db	2575	GCCCTGCATCCCTCTGGCCACAGATGATGTTCCAGAAATGATGGAACCAATTTTAATTTGT	2634
Oy	2635	ATATGTGATTTGTGTTAATATGTGAGGCGATCGGATCCGAGCTTAAACAATCATTTCTTT	2694
Db	2635	ATATGTGATTTGTGTTAATATGTGAGGCGATCGGATCCGAGCTTAAACAATCATTTCTTT	2694
Oy	2695	ACCCTCTCATGTGATACCCAAACCAAAATATGTTTACATTAATTTTGGATAGACAGATTACA	2754
Db	2695	ACCCTCTCATGTGATACCCAAACCAAAATATGTTTACATTAATTTTGGATAGACAGATTACA	2754
Oy	2755	AGCTTGTGAGAAAGTACTAGAGGATCATATATCAG	2788
Db	2755	AGCTTGTGAGAAAGTACTAGAGGATCATATATCAG	2788

XX	RESULT 5
XX	AAA88923
XX	ID AAA88923 standard; DNA; 2692 BP.
XX	AAA88923;
XX	05-MAR-2001 (first entry)
XX	Nucleotide sequence of CRYIA(c)-RTB2 fusion in pFASTBAC1.
XX	CRYIA(c); crystal protein; ricin toxin B; RTB2; lectin;
KW	insecticide; pesticide; toxin; transgenic plant; insect resistance;

Query Match	79.1%; Score 2204.6; DB 22; Length 2692;
Best Local Similarity	90.2%; Pred. No. 0;
Matches 2406; Conservative	0; Mismatches 249; Indels 12; Gaps 4;
1 AAATPAGATTATTTACTGTTTTCGTAACAGTTTGTATTAATAAAACCTATATAATTCGG 60	
1 AAATPAGATTATTTACTGTTTTCGTAACAGTTTGTATTAATAAAACCTATATAATTCGG 60	
61 GATTATTTATPACCGTCCACCATCGGGCGGGATTCGATGAGCAACAACCCAAACATCAAC 120	
61 GATTATTTATPACCGTCCACCATCGGGCGGGATTCGATGAGCAACAACCCAAACATCAAC 120	
121 GAATGCATTCATACCAACTGTTAGTAAACCCAGAGTTGAAGTACTTGGTGAACAAC 180	
121 GAATGCATTCATACCAACTGTTAGTAAACCCAGAGTTGAAGTACTTGGTGAACAAC 180	
181 ATTGAACACGGTTACATCCCATCGATGAGATCTCTGTCCTTGACAGATTCTGCTAGC 240	
181 ATTGAACACGGTTACATCCCATCGATGAGATCTCTGTCCTTGACAGATTCTGCTAGC 240	
241 GAGTTCGTCGACGAGTGTGGTGGTCTTCTCGAGATGATGACATCATCTGGGGTATCTTT 300	
241 GAGTTCGTCGACGAGTGTGGTGGTCTTCTCGAGATGATGACATCATCTGGGGTATCTTT 300	
301 GATCCATTCATAGGATGATCTCTGCTGCAAAATTGACAGTGTATCAACAGAGATC 360	
301 GATCCATTCATAGGATGATCTCTGCTGCAAAATTGACAGTGTATCAACAGAGATC 360	

OY	361	GAAAGATTCCGACGAAACAGGCCATCTCTAGTTTGGAAAGATTGAGCAATCTCTACCA	420
Db	361	GAAAGTTTCGACAGGAACAGGCCATCTCTAGTTTGGAAAGATTGAGCAATCTCTACCA	420
OY	421	ATCTATGACAGAGCTTCAGAGACTGGGAAGCCGATCCTACTAAACCAAGCTTCGCGAG	480
Db	421	ATCTATGACAGAGCTTCAGAGAGTGGGAAGCCGATCTTACTTAAACCAAGCTTCGCGAG	480
OY	481	GAAATGCGTATTCATTCACGACATGAAACAGGCCCTTGAACACAGATTCCTATGTC	540
Db	481	GAAATGCGTATTCATTCACGACATGAAACAGGCCCTTGAACACAGATTCCTATGTC	540
OY	541	GCAGTCCGAACCTACCAAGTCTCTCTGTTCCGTGTAAGTTCAAGAGCTAATCTTCAAC	600
Db	541	GCAGTCCGAACCTACCAAGTCTCTCTGTTCCGTGTAAGTTCAAGAGCTAATCTTCAAC	600
OY	601	CTCAGCGGCTTCGAGACGTTAGGGTGTGTTGGCAAGGTGGGAATTCGATGCTGCAC	660
Db	601	CTCAGCGGCTTCGAGACGTTAGGGTGTGTTGGCAAGGTGGGAATTCGATGCTGCAC	660
OY	661	ATCAATAGCCGTTTCAACGACCTTACTAGCTGATGGAACTACACGACCAAGCTGTT	720
Db	661	ATCAATAGCCGTTTCAACGACCTTACTAGCTGATGGAACTACACGACCAAGCTGTT	720
OY	721	CGTTGGTACAAACCTGGCTTGAAGCGTGTCTGGGGTCTGATTTCTAGAGATTGATTGA	780
Db	721	CGTTGGTACAAACCTGGCTTGAAGCGTGTCTGGGGTCTGATTTCTAGAGATTGATTGA	780
OY	781	TACAAACAGTTTACAGAGAAATTGACCCCTCACGTTTGGACATTTGTCTCTCCG	840
Db	781	TACAAACAGTTTACAGAGAAATTGACCCCTCACGTTTGGACATTTGTCTCTCCG	840
OY	841	AACTATGACTCCAGAACCTTACCTTACCGTACAGTGTCCCACTTACAGAGAAATCTAT	900
Db	841	AACTATGACTCCAGAACCTTACCTTACCGTACAGTGTCCCACTTACAGAGAAATCTAT	900
OY	901	ACTAACCCAGTTCTTGAGAACTTCGACGAGTTCGCGTGTCTGCCAAGTATCGAA	960
Db	901	ACTAACCCAGTTCTTGAGAACTTCGACGAGTTCGCGTGTCTGCCAAGTATCGAA	960
OY	961	GGCTTCATCAGAGGCCCACTTGAATGACATCTTGAAACAGCATTAATTTACACCGAT	1020
Db	961	GGCTTCATCAGAGGCCCACTTGAATGACATCTTGAAACAGCATTAATTTACACCGAT	1020
OY	1021	GCTCAGAGGAGATTAATTACTGCTGTGAGACCCGATCAAGGCCCTCCAGTTGGAATTC	1080
Db	1021	GCTCAGAGGAGATTAATTACTGCTGTGAGACCCGATCAAGGCCCTCCAGTTGGAATTC	1080
OY	1081	AGCGGGCCGAGTTTACCTTCTCTCTATGGAACTATGGGAAACGCCGCTCCACAACA	1140
Db	1081	AGCGGGCCGAGTTTACCTTCTCTCTATGGAACTATGGGAAACGCCGCTCCACAACA	1140
OY	1141	CGTATCGTTTGCTCAACTAGTCTAAGGTGTCTACAGAACCTTGTCTTCCACTTGTACGA	1200
Db	1141	CGTATCGTTTGCTCAACTAGTCTAAGGTGTCTACAGAACCTTGTCTTCCACTTGTACGA	1200
OY	1201	AGACCTTCAATATGCGTATCAACAACACAGCAACTTTCGTTCTTGACGGAACAGATTC	1260
Db	1201	AGACCTTCAATATGCGTATCAACAACACAGCAACTTTCGTTCTTGACGGAACAGATTC	1260
OY	1261	GCGTATGGAACCTCTTCTTAATCTTGCATCCGCTGTGTTACAGAAAGCGGAACGGTTGAT	1320
Db	1261	GCGTATGGAACCTCTTCTTAATCTTGCATCCGCTGTGTTACAGAAAGCGGAACGGTTGAT	1320
OY	1321	TCCTTGGAGAAATCCACACAGAAACAATGTGCCACCGGCAAGGATTTCTCCAC	1380
Db	1321	TCCTTGGAGAAATCCACACAGAAACAATGTGCCACCGGCAAGGATTTCTCCAC	1380
OY	1381	AGGTTGAGCAGAGTGCATGTTCCGTTCCGGATTCAAGAACAGTTCGCTGACATCATC	1440
Db	1381	AGGTTGAGCAGAGTGCATGTTCCGTTCCGGATTCAAGAACAGTTCGCTGACATCATC	1440
OY	1441	AGAGCTCTATGTTCTCATGATTCATCGTACGTGATTCGATTCACAAATATCATTCCTTC	1500

Db	1441	AGAGCTCTCTATGTTCTCTTGGATACACCGTAGTCTAGTTCAACAAACATCATCGCATCC	1500
Qy	1501	TCCTCAATATCACCCMAATCCCAATTGACCCAGTCTAACTAACCTTGGATCTGCAACTCTGTC	1560
Db	1501	GATAGTATTTACTCAAAATCCCTCGACAGTGAAG---GGAAACTTTTCTCTTCAACGGTCTGTGTC	1557
Qy	1561	GTCGAAGACACAGGCTTTCACAGAGTGATATTTCTTNGAAGAACTCTCTCGGCCAGATT	1620
Db	1558	ATTTTCAGGACCCAGGATTCACCTGGGAGAGCTCCTTAGACTCAACACAGTGGAAATTAAC	1617
Qy	1621	AGCACCTCAAGATTAACATCACTGCACCACTT---TCTCAAGATATTCGTGCAGATT	1677
Db	1618	ATTCAGAATAGAGGGATATATTGAAGTTTCCAAATTACTTCCATCACAATCTTACCAAGATAT	1677
Qy	1678	CGTTACCCATCTACCACTAACTTGCAAATTCGCACCTTCATCGACGGAAGGCCATACAT	1737
Db	1678	AGACTTGGTGTGAGAGTATGCTTCTGTGACCCCTTATCACCTCAACGGTAAATATGGGGTAAAT	1737
Qy	1738	CAGGGTAACTTCTCCGCAACCATCTCA---AGCGGACAGCACTTGCAAATCCGCACTTC	1794
Db	1738	TCATCCATCTTCTCCCAATACAGTTCCAGCTACACACTACCTCTTGGATTAATCTCCAAATCC	1797
Qy	1795	AGAACCGTCCGTTTCACTACTCCTTCAACTTCTCTAAGGATCAAGGATTTTCAACCTT	1854
Db	1798	AGCGATTTCCGTTACTTTGAAGGCCAATGCTTTTACATCTTCACTCGGTAAACATCTG	1857
Qy	1855	AGCCCTCATGTGTTCAATTTCTGGCAATGAAGTGTACATTTGACCCGTATTTGATTTGTGCT	1914
Db	1858	GGTTGTGAACACTTATAGTGGACATCGCAGAGTGAATTTTCACACAAATTCGATTCATTC	1917
Qy	1915	GCCGAAGTTACTTTCGAGGCTGAGTACTAGAAATTCATGCTGATGTTTGTATGTGATCCTG	1974
Db	1918	GTTACTGCAACACTCGAGGCTG---AATGAAATTAATGCTGATGTTTGTATGTGATCCTG	1974
Qy	1975	AGCCCTATGTGCTGATTCGTAGTGTGAATGGTCTATGTGTGATGTTAAGGATGGAAGAT	2034
Db	1975	AGCCCTATGTGCTGATTCGTAGTGTGAATGGTCTATGTGTGATGTTAAGGATGGAAGAT	2034
Qy	2035	TCCAACACGGAAACGCAATACAGTTGTGGCCATGCAAGTCTAATACAGATGCCAATCAGC	2094
Db	2035	TCCAACACGGAAACGCAATACAGTTGTGGCCATGCAAGTCTAATACAGATGCCAATCAGC	2094
Qy	2095	TCTGGACTTTGAAAAAGACAACTACTATTCGATCTAATGGAAGTGTAACTACTTAACG	2154
Db	2095	TCTGGACTTTGAAAAAGACAACTACTATTCGATCTAATGGAAGTGTAACTACTTAACG	2154
Qy	2155	GGTACAGTCCGGGAGTCTATGTGATGATCTATGATTCGAAATATCTCTGCCAATCTATGCCA	2214
Db	2155	GGTACAGTCCGGGAGTCTATGTGATGATCTATGATTCGAAATATCTCTGCCAATCTATGCCA	2214
Qy	2215	CCCGCTGGCAAAATATGGGATATATGGAACCATCATTAATCCGAGATCTAGTCTAGTTTAA	2274
Db	2215	CCCGCTGGCAAAATATGGGATATATGGAACCATCATTAATCCGAGATCTAGTCTAGTTTAA	2274
Qy	2275	CAGCGACATCAGGGAACAGTGTGACCACTTACCGTGCACAAACCAACTTTATGCGCTTAA	2334
Db	2275	CAGCGACATCAGGGAACAGTGTGACCACTTACCGTGCACAAACCAACTTTATGCGCTTAA	2334
Qy	2335	GTCGAAGTTGGCTTCTCTAATATATACAACTTTGTTTACAACTATGTTGGGCTAT	2394
Db	2335	GTCGAAGTTGGCTTCTCTAATATATACAACTTTGTTTACAACTATGTTGGGCTAT	2394
Qy	2395	ATGCTCTGTGCTTGCAAGCAAAATAGTGACAAGTATGAGATAGAGGACTGTAGCACTGAAA	2454
Db	2395	ATGCTCTGTGCTTGCAAGCAAAATAGTGACAAGTATGAGATAGAGGACTGTAGCACTGAAA	2454
Qy	2455	AGGCTGAACCAACAGTGGGCTCTTTATATGCAATGATGTTCAATACGTCCTAGCAGCAACCGAG	2514
Db	2455	AGGCTGAACCAACAGTGGGCTCTTTATATGCAATGATGTTCAATACGTCCTAGCAGCAACCGAG	2514
Qy	2515	ATTAATTGCTTACAAAGTATTTCTAATATACGGGAAAACGTTGTTAAGATCCTCTCTTGTG	2574
Db	2515	ATTAATTGCTTACAAAGTATTTCTAATATACGGGAAAACGTTGTTAAGATCCTCTCTTGTG	2574

Db	2515	ATAATGGCTTACAAGATGATTCCTAATATAGGGGAAACAGTTGTAAGATCCTCTTGTG	2574
Qy	2575	GGCCGTGACCTCTGGCCACGATGATGTTCAAGAAATGATGAACCATTTTAATTTGT	2634
Db	2575	GGCCTGATCCTCTGGCCACGATGATGTTCAAGAAATGATGAACCATTTTAATTTGT	2634
Qy	2635	ATAAGTGATTGGTGTAGATTGAGGC	2661
Db	2635	ATAAGTGATTGGTGTAGATTGAGGC	2661
RESULT 6			
AAAB8924	AAA8924 standard; DNA; 2436 BP.		
AAAB8924	AAA8924;		
AC	AAA8924;		
XX	05-MAR-2001 (first entry)		
DT	Nucleotide sequence of CryIA(c) -RTB3 fusion in pFASTBAC1.		
XX	CryIA(c); crystal protein; ricin toxin B; RTB3; lectin;		
XX	insecticide; pesticide; toxin; transgenic plant; insect resistance;		
KW	crop protection; pFASTBAC1; ds.		
OS	Chimeric - Bacillus thuringiensis.		
OS	Chimeric - Ricinus communis.		
OS	Chimeric - Baculovirus.		
XX	WO200066755-A2.		
PN	09-NOV-2000.		
XX	27-APR-2000; 2000WO-GB01633.		
PD	28-APR-1999; 99GB-0009796.		
XX	(PLAN-) PLANT BIOSCIENCE LTD.		
XX	Christou P, Mehlo L;		
PI	WPI; 2001-007228/01.		
XX	Novel nucleic acid molecule encoding a pesticidal fusion polypeptide		
PT	computing a toxin and a binding domain for producing transgenic plants		
PT	resistant to pests -		
XX	Claim 11; Fig 3k; 81pp; English.		
PS	This nucleotide sequence is that of a fusion between DNA encoding		
XX	crystal protein CryIA(c) (see AAA88915) of Bacillus thuringiensis and		
CC	DNA encoding ricin toxin B RTB3 (see AAA88918) in baculovirus transfer		
CC	vector pFASTBAC1, in which the fusion was cloned under the control		
CC	of the polyhedrin promoter. This is an example of claimed nucleic		
CC	acids encoding pesticidal fusion proteins between a toxin domain		
CC	and a heterologous binding domain capable of binding non-specifically		
CC	to a cell membrane without disrupting that membrane. The use of such		
CC	fusions may help to inhibit the acquisition of resistance in a pest		
CC	population treated with the protein. Vectors (e.g. baculovirus		
CC	vectors or vectors suitable for use in a plant), host cells, and		
CC	transgenic plants (especially rice or maize) are also provided.		
CC	Expression of the fusion protein in a plant is useful for influencing		
CC	or affecting the toxicity of a plant to a pest, allowing control of		
CC	e.g. Lepidoptera, Coleoptera, Culicidae, Simuliidae, Hymenoptera,		
CC	Homoptera, Diptera and Orthoptera pests.		
XX	Sequence 2436 BP; 660 A; 597 C; 527 G; 652 T; 0 other;		
SQ	Query Match 70.0%; Score 1952.8; DB 22; Length 2436;		
	Best Local Similarity 88.8%; Pred. No. 0;		
	Matches 2162; Conservative 0; Mismatches 262; Indels 12; Gaps 4		
Qy	1 AATAGTATTCTTACTGTTTGGTACAGCTTTGTGTAATATAAAAACTATAATATTCCG 60		

Ds	1	AAATBAGTATTTTACTGTTTTCTGTAACAGTTTGTGTAATAAAAAACTATATATTCGG	60
QY	61	GATTATTCATACCGTCCCAACCATCGGGGCGGGATTCATGCAACAAACCCAAATCAAC	120
Ds	61	GATTATTCATACCGTCCCAACCATCGGGGCGGGATTCATGCAACAAACCCAAATCAAC	120
QY	121	GAATGCATTCATACCACTGCTTGAGTAATCCCAAGTTGAATGTAATTTGGTGGAAACGC	180
Ds	121	GAATGCATTCATACCACTGCTTGAGTAATCCCAAGTTGAATGTAATTTGGTGGAAACGC	180
QY	181	ATTGAAACCGGTTACATCCCATGACATCTCTTGCTTGACACAGTTTCTCTCAAGC	240
Ds	181	ATTGAAACCGGTTACATCCCATGACATCTCTTGCTTGACACAGTTTCTCTCAAGC	240
QY	241	GAGTTCGTGCGAGGTGCTGGGTTGTTCTCGGACTAGTTGACATCATCTGGGGTATCTTT	300
Ds	241	GAGTTCGTGCGAGGTGCTGGGTTGTTCTCGGACTAGTTGACATCATCTGGGGTATCTTT	300
QY	301	GGTCCATTCATGGGATGATCTCTGCTGCAAAATTGACAGTTGATCAACCAAGATC	360
Ds	301	GGTCCATTCATGGGATGATCTCTGCTGCAAAATTGACAGTTGATCAACCAAGATC	360
QY	361	GAAAGTTGCGACAGGAACCAAGCCATCTGATGTTGAAAGATTGAGCAATCTGACCA	420
Ds	361	GAAAGTTGCGACAGGAACCAAGCCATCTGATGTTGAAAGATTGAGCAATCTGACCA	420
QY	421	ATCTATGACAGAGAGCTTCAGAGAGTGGGAACCCATCCTACTTAACCCAGCTCTCCGAG	480
Ds	421	ATCTATGACAGAGAGCTTCAGAGAGTGGGAACCCATCCTACTTAACCCAGCTCTCCGAG	480
QY	481	GAAATGCGTATTCATTTCAACGACATGAACAGCGCTTGACCAAGCTATCCATTTGTC	540
Ds	481	GAAATGCGTATTCATTTCAACGACATGAACAGCGCTTGACCAAGCTATCCATTTGTC	540
QY	541	GCAGTCCGAACCTAACAGTTCCTCTCTTGCCGCTGACTCAAGCAAGCTAATCTTCAC	600
Ds	541	GCAGTCCGAACCTAACAGTTCCTCTCTTGCCGCTGACTCAAGCAAGCTAATCTTCAC	600
QY	601	CTCAGCGTCTTCGAGAGCGTTAGCGTGTGTTGGGCAAAAGTGGGGATTGATGCTGCAAC	660
Ds	601	CTCAGCGTCTTCGAGAGCGTTAGCGTGTGTTGGGCAAAAGTGGGGATTGATGCTGCAAC	660
QY	661	ATCAATAGCCGTTTACACGACCTTACTAGGCTGATTGGAACCTAACCCGACCGCTGTT	720
Ds	661	ATCAATAGCCGTTTACACGACCTTACTAGGCTGATTGGAACCTAACCCGACCGCTGTT	720
QY	721	CGTTGGTATACACCTGCGCTTGGAGCGGTCTGCGGTCCTGATTTCTAGAGATTGATTTGA	780
Ds	721	CGTTGGTATACACCTGCGCTTGGAGCGGTCTGCGGTCCTGATTTCTAGAGATTGATTTGA	780
QY	781	TACACCAAGTTCAGAGAGAAATTGACCTCAGAGTTTGGACATGTGCTCTCTTCCCG	840
Ds	781	TACACCAAGTTCAGAGAGAAATTGACCTCAGAGTTTGGACATGTGCTCTCTTCCCG	840
QY	841	AACATAGACTCCAGAACCTTACCCTATCCGTAACAGTGTCCCACTTACAGAGAAATCTAT	900
Ds	841	AACATAGACTCCAGAACCTTACCCTATCCGTAACAGTGTCCCACTTACAGAGAAATCTAT	900
QY	901	ACTAACCCAGTCTTGAGAACCTTCAACGCTTACGATGCTTCCGCTTCCCAAGTATCGAA	960
Ds	901	ACTAACCCAGTCTTGAGAACCTTCAACGCTTACGATGCTTCCGCTTCCCAAGTATCGAA	960
QY	961	GGCTCCATCAGGAGGCCAAGCTTGATGGAACATCTTGAAACAGATTAATCTACACCGAT	1020
Ds	961	GGCTCCATCAGGAGGCCAAGCTTGATGGAACATCTTGAAACAGATTAATCTACACCGAT	1020
QY	1021	GCTCAAGAGAGAGATTAATCTGATCTGGAACACAGATCATGCGCTCTCCAGTTGGATTC	1080
Ds	1021	GCTCAAGAGAGAGATTAATCTGATCTGGAACACAGATCATGCGCTCTCCAGTTGGATTC	1080
QY	1081	ACGGGGCCGAGTTTACCTTCTCTCTATGGAACATATGGGAACGGCGCTCCAAACAAC	1144

Db 1081 AGCGGCCCGAGTTTACCTTCTCTCTATGGAATATGGAAGCCCGCTCCACAA 1140
 Qy 1141 CGTATCGTGTCTCACTAGGTAGGAGGTGTCTACAGAACTTGTCTTCCACTTTAGAGA 1200
 Db 1141 CGTATCGTGTCTCACTAGGTAGGAGGTGTCTACAGAACTTGTCTTCCACTTTAGAGA 1200
 Qy 1201 AGACCTTCAATATCGGTATCAACAACAGCACTTTCGTTTGAAGCAAGAGTTT 1260
 Db 1201 AGACCTTCAATATCGGTATCAACAACAGCACTTTCGTTTGAAGCAAGAGTTT 1260
 Qy 1261 GCCATATGAACTCTTCTAATTTCCATCCGCTGTTTACAGAAAGAGGGAACCGTTGAT 1320
 Db 1261 GCCATATGAACTCTTCTAATTTCCATCCGCTGTTTACAGAAAGAGGGAACCGTTGAT 1320
 Qy 1321 TCTTGGACGAAATCCCAACAGCAACAAATGTGCCACCCGAGCAAGATTTCTCCAC 1380
 Db 1321 TCTTGGACGAAATCCCAACAGCAACAAATGTGCCACCCGAGCAAGATTTCTCCAC 1380
 Qy 1381 AGGTTGAGCCACGTGTCCATGTTCCGTTCCGGAATTCAGCAACAGTTCCGTGAGCATATC 1440
 Db 1381 AGGTTGAGCCACGTGTCCATGTTCCGTTCCGGAATTCAGCAACAGTTCCGTGAGCATATC 1440
 Qy 1441 AGAGCTCTATGTTCTCATGATTCATGTAGTGTGATTCACAAATATCATTCCTTCC 1500
 Db 1441 AGAGCTCTATGTTCTCATGATTCATGTAGTGTGATTCACAAATATCATTCCTTCC 1500
 Qy 1501 TCTCAAAATCAACCAAAATCCCAATTCAGCAACCACTTGGATCTGAACTTCTGTC 1560
 Db 1501 GATAGTATTAATCAAAATCCCAATTCAGCAACCACTTGGATCTGAACTTCTGTC 1560
 Qy 1561 GTGAAGGACACGAGCTTCAACAGAGGTGATATCTTGAAGAACTTCTCTGCGCAGATT 1620
 Db 1561 GTGAAGGACACGAGCTTCAACAGAGGTGATATCTTGAAGAACTTCTCTGCGCAGATT 1620
 Qy 1621 AGACCTCTAGAGTTAATCATCTGACATCTTCAAGATCTGATCTGATCTGATCTGAT 1677
 Db 1621 AGACCTCTAGAGTTAATCATCTGACATCTTCAAGATCTGATCTGATCTGATCTGAT 1677
 Qy 1678 CGTTACGATCTACCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1737
 Db 1678 AGAGTTGCTGTGAGGATGATCTTCTGTGACCCCTATTCATCTCAACGTTAATTTGGGATAT 1737
 Qy 1738 CAGGATTAATCTTCTCGCAACCATATGCA--AGCGGACAGCACTTGGCAATCCGAGCTTC 1794
 Db 1738 TCATTCATCTTCTCGCAACCATATGCA--AGCGGACAGCACTTGGCAATCTCCAAATCC 1794
 Qy 1795 AGAACCGTGGTTCATCTCTTCTTCACTTCTTCACTTCTTCACTTCTTCACTTCTTCACTT 1854
 Db 1795 AGAACCGTGGTTCATCTCTTCTTCACTTCTTCACTTCTTCACTTCTTCACTTCTTCACTT 1854
 Qy 1855 AGCGCTCATGTCTTCAATTTCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 1914
 Db 1855 AGCGCTCATGTCTTCAATTTCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 1914
 Qy 1915 GCCCAAGTTACCTTCAAGCTGAGTACTGAGAAATTCATGCTGATGTTTGAATGATCTGTG 1974
 Db 1915 GTTACTGCAACACTCTGAGGCTG---AATGAAATTCATGCTGATGTTTGAATGATCTGTG 1974
 Qy 1975 AGCCCATATGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2034
 Db 1975 AGCCCATATGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2034
 Qy 2035 TCCCAACGGAAGCAATATAGTTGTGCGCATGCAATCTTAATCAATGCAATGCAATGCAAT 2094
 Db 2035 TCCCAACGGAAGCAATATAGTTGTGCGCATGCAATCTTAATCAATGCAATGCAATGCAAT 2094
 Qy 2095 TCTGGAATTTGAAAAGAGCAATATCTTCAATGAAAGTGTTTAACTTACTTACG 2154
 Db 2095 TCTGGAATTTGAAAAGAGCAATATCTTCAATGAAAGTGTTTAACTTACTTACG 2154
 Qy 2155 GGTACAGTCCGGAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2214
 Db 2155 GGTACAGTCCGGAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2214

Qy 2215 CCCGCTGGCAAAATATGGAATATGGAACCATATGAAATCCCAATCTAGTCTAGTCTTATG 2274
 Db 2215 CCCGCTGGCAAAATATGGAATATGGAACCATATGAAATCCCAATCTAGTCTAGTCTTATG 2274
 Qy 2275 CAGGACATCAAGGAACAGTGTGTCACACTTAAAGGTGCAAAACCAATTTATCCCTTA 2334
 Db 2275 CAGGACATCAAGGAACAGTGTGTCACACTTAAAGGTGCAAAACCAATTTATCCCTTA 2334
 Qy 2335 GTCAAGGTGGCTTCTTACTAATATATACAACTTTGTTTGAACCAATTTGTTGAGCTAT 2394
 Db 2335 GTCAAGGTGGCTTCTTACTAATATATACAACTTTGTTTGAACCAATTTGTTGAGCTAT 2394
 Qy 2395 ATGCTGTGCTTCAAGCAAAATAGTGAACAGTAT 2430
 Db 2395 ATGCTGTGCTTCAAGCAAAATAGTGAACAGTAT 2430
 RESULT 7
 ID AAA88914
 AAA88914 standard; DNA; 2062 BP.
 AC AAA88914;
 DT 05-MAR-2001 (first entry)
 XX Nucleotide sequence of CryIA(b) in pFASTBAC1.
 DE CryIA(b); crystal protein; insecticide; pesticide; toxin;
 KW transgenic plant; insect resistance; crop protection; pFASTBAC1;
 KM ds.
 XX Chimeric - Bacillus thuringiensis.
 OS Chimeric - Baculovirus.
 XX Key Location/Qualifiers
 FT CDS 97..194
 FT /*tag= a
 PN WO20066755-A2.
 XX 09-NOV-2000.
 PD 27-APR-2000; 2000WO-GB01633.
 XX 28-APR-1999; 99GB-0009796.
 PR (PLAN-) PLANT BIOSCIENCE LTD.
 XX Christou P, Mehlo L;
 PI WPI: 2001-007228/01.
 DR Novel nucleic acid molecule encoding a pesticidal fusion polypeptide
 XX comprising a toxin and a binding domain for producing transgenic plants
 PT resistant to pests -
 XX
 PS Claim 9; Fig 3a; 81pp; English.
 CC The present sequence is that of Bacillus thuringiensis crystal
 CC protein CryIA(b) DNA in baculovirus transfer vector pFASTBAC1, in
 CC which the gene was cloned under the control of the polyhedrin
 CC promoter. The invention provides nucleic acids (see AAA88919-24)
 CC encoding pesticidal fusion proteins comprising a toxin domain and a
 CC heterologous binding domain capable of binding non-specifically to
 CC a cell membrane without disrupting that membrane. The toxin domain
 CC is preferably obtained from CryIA(b) or CryIA(c), and the binding
 CC domain is preferably derived from a lectin, such as ricin toxin B
 CC chain. The use of such fusions may help to inhibit the acquisition
 CC of resistance in a pest population treated with the protein.
 CC Vectors (e.g. baculovirus vectors or vectors suitable for use in a
 CC plant), host cells, and transgenic plants (especially rice or
 CC maize) are also provided. Expression of the fusion protein in a

ID	AA075466	standard; DNA; 7378 BP.
XX		
AC	AA075466;	
XX		
DT	15-JAN-2001	(first entry)
XX		
DE	Complete nucleotide sequence of plasmid pZO1502.	
XX		
KW	35S promoter; alcohol dehydrogenase intron; nopaline synthase terminator;	
KW	insecticidal Cry IAb protein toxin; transgenic plant; fungal toxin;	
XX	afatoxin; baculovirus; Lepidopteran insect; glufosinate; ds.	
XX		
OS	Synthetic.	
XX		
PN	US6114608-A.	
XX		
PD	05-SEP-2000.	
XX		
XX	13-MAR-1998;	98US-0042426.
PF		
XX		
PR	14-MAR-1997;	97US-0109808.
XX		
PA	(NOVS) NOVARTIS AG.	
XX		
PI	Dietrich PS, Mettler IJ, Simibaldi RM;	
XX		
DR	WPI; 2000-586487/55.	
XX		
PT	Novel DNA construct comprising an expression cassette having a	
XX	functional constitutive promoter, operably linked to a maize alcohol	
XX	dehydrogenase intron, gene encoding Cry IAb protein and a terminator	-
PS	Example 1; Column 25-32; 24pp; English.	
XX		
CC	The present sequence represents plasmid pZO1502, which is a vector	
CC	of the invention. The specification describes a nucleic acid construct,	
CC	comprising an expression cassette containing a cauliflower mosaic virus	
CC	(CaMV) 35S promoter, a maize alcohol dehydrogenase intron, a DNA molecule	
CC	encoding an insecticidal Cry IAb protein toxin and a NOS (nopaline	
CC	synthase) terminator in operable linkage. The nucleic acid constructs	
CC	are useful for producing transgenic plants such as maize, wheat, barley,	
CC	sorghum and rice. Preferably, maize plants such as field corn, sweet	
CC	corn, white corn, silage corn or popcorn are produced. The transgenic	
CC	maize is used for preparing food materials with reduced levels of fungal	
CC	toxins, e.g. aflatoxin. The transgenic plants express a baculovirus	
CC	crystal protein toxin, which is effective against lepidopteran insects at	
CC	relatively high levels and further provides resistance to the	
CC	non-selective herbicide glufosinate.	
XX		
XX		
SQ	Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other;	
	Query Match 66.3%; Score 1848.2; DB 21; Length 7378;	
	Best Local Similarity 99.6%; Pred. No. 0;	
	Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
QY	95	CCATGACAACCAACCAACATCAACGATGCATTCATACACTGCTTGATTAACCCAG 154
DB	1020	CCATGACAACCAACCAACATCAACGATGCATTCATACACTGCTTGATTAACCCAG 1079
QY	155	AAAGTTGAAGTACTTGGTGGAGAACCCATTGAAACCGGTTTACACTCCATCGACATCTCT 214
DB	1080	AAAGTTGAAGTACTTGGTGGAGAACCCATTGAAACCGGTTTACACTCCATCGACATCTCT 1139
QY	215	TGTCCTTGACACAGTTTCGCTGCAGCGAGTTGTCGCAAGGTCGCTGGTTCGTTCCGAG 274
DB	1140	TGTCCTTGACACAGTTTCGCTGCAGCGAGTTGTCGCAAGGTCGCTGGTTCGTTCCGAG 1139
QY	275	TAGTTGACATCATCTGGGGTATCTTTGGTTCATCTCAATGGGATCATTCCTGTCGACAA 334
DB	1200	TAGTTGACATCATCTGGGGTATCTTTGGTTCATCTCAATGGGATCATTCCTGTCGTCGACAA 1259
QY	335	TTGAGCAGTTGATCAACCAAGAGATCGAAGATTTGCCAGGAAACGAGCCATCTTAGCT 394

Db	1260	TTGAGCAGTGTGATCAACACAGAGATCGAAGAGTTCCGACAGAAACACAGGCATCTTAGGT	1319
Oy	395	TGGAAGATTGAGCAATCTCTACCAATCTATGCAAGAGCTTCAGAGGTGGAGCCG	454
Db	1320	TGGAAGATTGAGCAATCTCTACCAAAATCTATGCAAGAGAGCTTCAGAGAGTGGAGACCG	1379
Oy	455	ATCTACTTAACCCAGCCTCCGCGAAGGAATAGCGTATTCAATTCAAGACATGAACACGG	514
Db	1380	ATCTACTTAACCCAGCCTCCGCGAAGGAATAGCGTATTCAATTCAAGACATGAACACGG	1439
Oy	515	CCTTGACCAACAGCATATCCCAATTTGTTCCAGTCCAGAACTACCAAGTTCTTCTTGTCG	574
Db	1440	CCTTGACCAACAGCATATCCCAATTTGTTCCAGTCCAGAACTACCAAGTTCTTCTTGTCG	1499
Oy	575	TGTACGTTCAAGCAGTAATCTTCACTCAGCCTGCTTGGAGAGCGTTAGCGTGTGGG	634
Db	1500	TGTACGTTCAAGCAGTAATCTTCACTCAGCCTGCTTGGAGAGCGTTAGCGTGTGGG	1559
Oy	635	AAAGGTGGGATTTGATGCTGCAACCATTCATTAACCGTTACAAAGACTTACTAGGCTGA	694
Db	1560	AAAGGTGGGATTTGATGCTGCAACCATTCATTAACCGTTACAAAGACTTACTAGGCTGA	1619
Oy	695	TTGGAACCTACACGACCAACGCGCTTGTTGGTGTCAACACCTGGCTGGAGCGTCTGG	754
Db	1620	TTGGAACCTACACGACCAACGCGCTTGTTGGTGTCAACACCTGGCTGGAGCGTCTGG	1679
Oy	755	GTCCTGATTTAGAGATTGAGATTAGATACACAGTTTCAGAGAGAAATGACCTTCACAG	814
Db	1680	GTCCTGATTTAGAGATTGAGATTAGATACACAGTTTCAGAGAGAAATGACCTTCACAG	1739
Oy	815	TTTTGGACATTTGTCTCTCTTCCCGAATCTATGACTCCAGAACCTACCTATCCGTACAG	874
Db	1740	TTTTGGACATTTGTCTCTCTTCCCGAATCTATGACTCCAGAACCTACCTATCCGTACAG	1799
Oy	875	TGTCCCAACCTTACAGAGAAATCTATCTAACCCAGTCTTGAGAACCTTCGACGGTACT	934
Db	1800	TGTCCCAACCTTACAGAGAAATCTATCTAACCCAGTCTTGAGAACCTTCGACGGTACT	1855
Oy	935	TCCGTGTCTTCCCAAGATTCGAAGGCTTCATCAGGAGCCCACTTGATGACATCT	994
Db	1860	TCCGTGTCTTCCCAAGATTCGAAGGCTTCATCAGGAGCCCACTTGATGACATCT	1919
Oy	995	TGAACAGCATATCTATCTACACCGATGCTCACAAGAGAGATTTACTGTCTGACACC	1055
Db	1920	TGAACAGCATATCTATCTACACCGATGCTCACAAGAGAGATTTACTGTCTGACACC	1979
Oy	1055	AGATCAGCGCCTCCACGTTGGATTTCAAGCGGCGCGAGTTTAACTTCTCTCTATGGAA	1114
Db	1980	AGATCAGCGCCTCCACGTTGGATTTCAAGCGGCGCGAGTTTAACTTCTCTCTATGGAA	2033
Oy	1115	CTATGGGAAACGCGCGCTCACAACAACCTATGTTGCTCAACTAGAGTCAAGGTGTCTACA	1174
Db	2040	CTATGGGAAACGCGCGCTCACAACAACCTATGTTGCTCAACTAGAGTCAAGGTGTCTACA	2099
Oy	1175	GAACTTGTCTTCAACTTGTATCAGAGAACCTTTCATATGGGTATCAACAACGACAAAC	1233
Db	2100	GAACTTGTCTTCAACTTGTATCAGAGAACCTTTCATATGGGTATCAACAACGACAAAC	2155
Oy	1235	TTTCGGTCTTGAAGGAAACAGAGTTCCGCTATGGAACCTCTTCAACTTGGCATCCGCTG	1294
Db	2160	TTTCGGTCTTGAAGGAAACAGAGTTCCGCTATGGAACCTCTTCAACTTGGCATCCGCTG	2215
Oy	1295	TTTACAGAAAGAGCGGAACCGTTGATTTCTTGGAGAAATCCACACAGAACCAATG	1355
Db	2220	TTTACAGAAAGAGCGGAACCGTTGATTTCTTGGAGAAATCCACACAGAACCAATG	2277
Oy	1355	TGCCACCCAGGCAAGGATTTCTTCCACAGAGTTGAGCCACAGTCCATGTTCCGTTCCGAT	1411
Db	2280	TGCCACCCAGGCAAGGATTTCTTCCACAGAGTTGAGCCACAGTCCATGTTCCGTTCCGAT	2333
Oy	1415	TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCCATATTTCTCATGATTCATCGTAGTG	1474
Db	2340	TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCCATATTTCTCATGATTCATCGTAGTG	2399


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Db      1620 TTGAAATCTACACCGACCCGCTGCTTGTGTAACAACACCTGGGTGGAGGTGTCTGGG 1679
Qy      755 GTCCGATTTCTAGAGATTGATGATTAACAACAGTTGAGAGAAATTGACCCCTCACAG 814
Db      1680 GTCCGATTTCTAGAGATTGATGATTAACAACAGTTGAGAGAAATTGACCCCTCACAG 1739
Qy      815 TTTTGACATTTGTCTCTCTCTCCGGAATATGACTCCAGAACCTTACCTTACCGTACAG 874
Db      1740 TTTTGACATTTGTCTCTCTCTCCGGAATATGACTCCAGAACCTTACCTTACCGTACAG 1799
Qy      875 TGTCCCACTTACACGAGAAATCTATATAACCCAGTTCTTGAGAACTTGACGGTACT 934
Db      1800 TGTCCCACTTACACGAGAAATCTATATAACCCAGTTCTTGAGAACTTGACGGTACT 1859
Qy      935 TCCGTGTTCTGCCCAAGGTATGCAAGGCTCATAGAGGCCACACTTGATGACATCT 994
Db      1860 TCCGTGTTCTGCCCAAGGTATGCAAGGCTCATAGAGGCCACACTTGATGACATCT 1919
Qy      995 TGAACAGCATTAATCTATACACCGATGCTCAGAGAGAGATATTACTGTCTGGACAC 1054
Db      1920 TGAACAGCATTAATCTATACACCGATGCTCAGAGAGAGATATTACTGTCTGGACAC 1979
Qy      1055 AGATCATGCGCTCTTCAGTTGATTCAGCGGCGCCGAGTTTACCTTCTCTCTATGGA 1114
Db      1980 AGATCATGCGCTCTTCAGTTGATTCAGCGGCGCCGAGTTTACCTTCTCTCTATGGA 2039
Qy      1115 CTATGGGAAAGCGCGCTCACAACAGGTATCGTTGCTCACTAGGTAGGTGTCTACA 1174
Db      2040 CTATGGGAAAGCGCGCTCACAACAGGTATCGTTGCTCACTAGGTAGGTGTCTACA 2099
Qy      1175 GAACCTGTCTCCCACTTGTACAGAAAGACCTTCAATATGCGTATCAACAACAGCAAC 1234
Db      2100 GAACCTGTCTCCCACTTGTACAGAAAGACCTTCAATATGCGTATCAACAACAGCAAC 2159
Qy      1235 TTTCCGTTCTTGACGGAACAGAGTTGCGCTATGGAACCTCTTCTACTTCCATCCGCTG 1294
Db      2160 TTTCCGTTCTTGACGGAACAGAGTTGCGCTATGGAACCTCTTCTACTTCCATCCGCTG 2219
Qy      1295 TTTACAGAAAGCGGGAACCGGTGATTCCTTGAGAGAAATCCACACAGAAACAATG 1354
Db      2220 TTTACAGAAAGCGGGAACCGGTGATTCCTTGAGAGAAATCCACACAGAAACAATG 2279
Qy      1355 TGCCACCCAGGCAAGAGTTCTCCACAGGTTGAGCCAGGTGTCACTGTTCCGTTCCGAT 1414
Db      2280 TGCCACCCAGGCAAGAGTTCTCCACAGGTTGAGCCAGGTGTCACTGTTCCGTTCCGAT 2339
Qy      1415 TCAGCAACAGTTCCTGAGCATCATCAAGCTCTATGTTCTCATGATTCATCGTAGTG 1474
Db      2340 TCAGCAACAGTTCCTGAGCATCATCAAGCTCTATGTTCTCATGATTCATCGTAGTG 2399
Qy      1475 CTGAGTTCAACAATTCATTCCTCTCTCAAAATCAACCAATCCCATTTGACCAAGTCA 1534
Db      2400 CTGAGTTCAACAATTCATTCCTCTCTCAAAATCAACCAATCCCATTTGACCAAGTCTA 2455
Qy      1535 CTAACCTTGATCTGGAACCTTCTGCTGAAAGGACAGAGCTTCAAGAGGTGATATTC 1594
Db      2460 CTAACCTTGATCTGGAACCTTCTGCTGAAAGGACAGAGCTTCAAGAGGTGATATTC 2519
Qy      1595 TTAGAAGAACTTCTCTGCGCCAGATTAGACCCCTCAGAGTTTAACTACTGACCACTTT 1654
Db      2520 TTAGAAGAACTTCTCTGCGCCAGATTAGACCCCTCAGAGTTTAACTACTGACCACTTT 2579
Qy      1655 CTCAAGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1714
Db      2580 CTCAAGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2639
Qy      1715 CCATGACGGAAGGCTTATCAATCAAGGTTACTTCTCGCAACAATGTCAGCGGACAGA 1774
Db      2640 CCATGACGGAAGGCTTATCAATCAAGGTTACTTCTCGCAACAATGTCAGCGGACAGA 2699
Qy      1775 ACTTGCAATCGGCGAGCTTCAAGACCGGTGTTTCACTACTCTTCAACTTCTTAACG 1834

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Db      2700 ACTTGCAATCGGCGAGCTTCAAGAACGTCGGTTCACTACTCTTTCAACTTCTTAACG 2759
Qy      1835 GATCAAGCGTTTTCACCCCTTAGCGCTCATGTTCAATTCTGCAATGAAGTATACATTG 1894
Db      2760 GATCAAGCGTTTTCACCCCTTAGCGCTCATGTTCAATTCTGCAATGAAGTATACATTG 2819
Qy      1895 ACCGTATTGAGTTTGTCTGCGCGAAGTTACCTTGAGGCTGAGTACTGAGAAATTCATGC 1954
Db      2820 ACCGTATTGAGTTTGTCTGCGCGAAGTTACCTTGAGGCTGAGTACTGAGAAATTCATGC 2879
Qy      1955 T 1955
Db      2880 T 2880

RESULT 10
ID AAD06368
ID AAD06368 standard; DNA; 7378 BP.
XX
AC AAD06368;
XX
DT 10-AUG-2001 (first entry)
XX
DE Plasmid pZO1502 comprising Btk and Pat gene expression cassettes.
XX
KW Maize; expression cassette; 35S promoter; alcohol dehydrogenase intron;
KW crystal 1ab; CryIAb toxin; phosphinothricin acetyl transferase; PAT;
KW nopaline synthase; NOS terminator; aflatoxin; food material;
KW sweet corn; human food; plasmid pZO1502; de.
XX
OS Chimeric - Zea mays.
OS Chimeric - Cauliflower mosaic virus.
OS Chimeric - Bacillus thuringiensis.
OS Chimeric - Streptomyces sp.
XX
FH Key
FT misc_feature
FT /tag= a
FT /note= "Corresponds to Bt CryIAb toxin DNA"
FT /tag= b
FT /note= "Corresponds to Pat gene"
FT misc_feature
FT /tag= b
FT /note= "Corresponds to beta-lactamase gene"

US6229075-B1.
PD 08-MAY-2001.
XX
PF 11-JUN-1999; 99US-0330760.
XX
PR 14-MAR-1997; 97US-0109808.
PR 13-MAR-1998; 98US-0042426.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Mettler ID, Plaisted DC, Grier SL, Houghton W, Gardiner M;
XX
WP1: 2001-342708/36.
XX
PT New maize (Zea mays) inbred line R412H (ATCC 209675), useful for
PT producing corn with reduced levels of toxins (e.g. the fungal
PT aflatoxin) and for preparing food materials for human or animal
PT consumption -
XX
PS Example 1; Column 21-28; 30pp; English.
XX
CC The present invention relates to maize inbred line R412H which comprises
CC a nucleic acid construct with two cassettes, which are transcribed in the
CC same direction. The expression cassette comprises a Cauliflower mosaic
CC virus (CaMV) 35S constitutive promoter operably linked to a maize alcohol
CC dehydrogenase intron, a DNA sequence of a gene encoding a

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CC Bacillus thuringiensis (Bt) crystal 1Ab (CryIAb) toxin or
 CC phosphinothricin acetyl transferase (PAT) and a nopaline synthase (NOS)
 CC terminator functional in plants. The maize induced line R412H is useful
 CC for producing corn with reduced levels of toxins (e.g. the fungal
 CC aflatoxin). This maize line is particularly useful for preparing food
 CC materials for human or animal consumption, e.g. sweet corn for
 CC packaging or fresh use as human food, or grain or silage made from field
 CC corn. The present sequence is plasmid p201502. The plasmid
 CC comprises the base plasmid vector and an expression cassette for the Btk
 CC gene and pat gene, which is related to the invention.

SO Sequence 7378 Bp; 1917 A; 1803 C; 1719 G; 1939 T; 0 other:

Query Match 66.3%; Score 1848.2; DB 22; Length 7378;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 95 CCATGACACACACCCAAACATCAACGAATGATTCCTATACACTGCTTGAGTAACCG 154
 DB 1020 CCATGACACACACCCAAACATCAACGAATGATTCCTATACACTGCTTGAGTAACCG 1079
 QY 155 AAGTTGAAGTACTGGTGGAGACGATGAAACCGGTTACACTCCCATGACATCTCCT 214
 DB 1080 AAGTTGAAGTACTGGTGGAGACGATGAAACCGGTTACACTCCCATGACATCTCCT 1139
 QY 215 TGTCCTTGACACAGTTTCTGCTCAGCGAGTTGCTGCGAGTGTGGATTGCTTCGAG 274
 DB 1140 TGTCCTTGACACAGTTTCTGCTCAGCGAGTTGCTGCGAGTGTGGATTGCTTCGAG 1139
 QY 275 TAGTTGACATCATCTGGGGGATCTTTTGGTCCATCTCAATGGGATGCAATTCCTGGTGA 334
 DB 1200 TAGTTGACATCATCTGGGGGATCTTTTGGTCCATCTCAATGGGATGCAATTCCTGGTGA 1259
 QY 335 TTGACAGATTGATCAACACGAGATCGAAGAGTTGGCCAGGAACGAGGCCATCTTAGT 394
 DB 1260 TTGACAGATTGATCAACACGAGATCGAAGAGTTGGCCAGGAACGAGGCCATCTTAGT 1319
 QY 395 TGAAGATTGAGCAATCTCTCAAAATCTATGACAGAGCTTCGAGAGTGGGAAGCCG 454
 DB 1320 TGAAGATTGAGCAATCTCTCAAAATCTATGACAGAGCTTCGAGAGTGGGAAGCCG 1379
 QY 455 ATCTCACTAACCCAGCTCTCCGCGAGAAATGCCATTCATTTCAACGACATGAACACG 514
 DB 1380 ATCTCACTAACCCAGCTCTCCGCGAGAAATGCCATTCATTTCAACGACATGAACACG 1439
 QY 515 CTTGACACAGCTATCCCATTTGTCGAGATCCAGAACTAACCAATGTTCTCTTGTGCG 574
 DB 1440 CTTGACACAGCTATCCCATTTGTCGAGATCCAGAACTAACCAATGTTCTCTTGTGCG 1499
 QY 575 TGTACGTTCAAGCAGCTAATCTTCACTCAGCGTCTTCGAGACGTTAGCGTGTGGGC 634
 DB 1500 TGTACGTTCAAGCAGCTAATCTTCACTCAGCGTCTTCGAGACGTTAGCGTGTGGGC 1559
 QY 635 AAAGGTGGGATTCGATGCTGCAACATCAATAGCCGTTTCAACGACCTTACTAGGCTGA 694
 DB 1560 AAAGGTGGGATTCGATGCTGCAACATCAATAGCCGTTTCAACGACCTTACTAGGCTGA 1619
 QY 695 TTGGAACCTACACGACGCTGTTGCTGGTGAACAACACTGCTGGAGCGTGTGCGG 754
 DB 1620 TTGGAACCTACACGACGCTGTTGCTGGTGAACAACACTGCTGGAGCGTGTGCGG 1679
 QY 755 GTCTGATTTAGAGATTGATTGATTAACAACCAAGTTCCGAGAGAAATTGACCTTCAG 814
 DB 1680 GTCTGATTTAGAGATTGATTGATTAACAACCAAGTTCCGAGAGAAATTGACCTTCAG 1739
 QY 815 TTTTGGACATTTGCTCTCTCCGAACTATGACTCCAGAACCTTACCTATCCGTAGAG 874
 DB 1740 TTTTGGACATTTGCTCTCTCCGAACTATGACTCCAGAACCTTACCTATCCGTAGAG 1799
 QY 875 TGTCCCACTTACAGAGAAATCTATACTAACCCAGATTCTTGAGAACTTGCAGCGTAGCT 934
 DB 1800 TGTCCCACTTACAGAGAAATCTATACTAACCCAGATTCTTGAGAACTTGCAGCGTAGCT 1859

QY 935 TCCGTGTTCTGCCCAAGGATATGGAAGGCTCCATCAGAGACCCCACTTGTATGACATCT 994
 DB 1860 TCCGTGTTCTGCCCAAGGATATGGAAGGCTCCATCAGAGACCCCACTTGTATGACATCT 1919
 QY 995 TGAACACATTAATCTATACACGATGCTCAGACAGAGAGATTTACTGTGCTGACACC 1054
 DB 1920 TGAACACATTAATCTATACACGATGCTCAGACAGAGAGATTTACTGTGCTGACACC 1979
 QY 1055 AGATCATGCGCTCCAGTTGATTCAGCGGGCCGAGTTTACCTTCTCTATAGAA 1114
 DB 1980 AGATCATGCGCTCCAGTTGATTCAGCGGGCCGAGTTTACCTTCTCTATAGAA 2039
 QY 1115 CTATGGGAAACCGGCTCCACACACAGTATCGTTGCTCAACTATGATGAGGTCTTACA 1174
 DB 2040 CTATGGGAAACCGGCTCCACACACAGTATCGTTGCTCAACTATGATGAGGTCTTACA 2099
 QY 1175 GAACCTTGCTCCACCTTGATCAGAGACCCCTCAATATCGGATCAACACAGCAAC 1234
 DB 2100 GAACCTTGCTCCACCTTGATCAGAGACCCCTCAATATCGGATCAACACAGCAAC 2159
 QY 1235 TTTCCGTTCTTGAACGAAACAGAGTTCCGCTATAGGAACCTTCTTACTTGGCATCCG 1294
 DB 2160 TTTCCGTTCTTGAACGAAACAGAGTTCCGCTATAGGAACCTTCTTACTTGGCATCCG 2219
 QY 1295 TTTACAGAAAGCGGAAACGTTGATTCCTTGGACGAAATCCACACAGAAACAATG 1354
 DB 2220 TTTACAGAAAGCGGAAACGTTGATTCCTTGGACGAAATCCACACAGAAACAATG 2279
 QY 1355 TGCCACCCAGGCAAGATTTCCGCCAGTTGACCCAGTTCATGTTCCGTTCCGGAT 1414
 DB 2280 TGCCACCCAGGCAAGATTTCCGCCAGTTGACCCAGTTCATGTTCCGTTCCGGAT 2339
 QY 1415 TCAGCAACAGTTCGATGATCATCAAGCTCTATGTTCTCATGGAATTCATGATG 1474
 DB 2340 TCAGCAACAGTTCGATGATCATCAAGCTCTATGTTCTCATGGAATTCATGATG 2399
 QY 1475 CTGAGTTCAACAAATATCTTCTCTCTCAAAATCCCAATTCCTTCAATGCAAGCTA 1534
 DB 2400 CTGAGTTCAACAAATATCTTCTCTCTCAAAATCCCAATTCCTTCAATGCAAGCTA 2459
 QY 1535 CTAACCTTGGATCTGGAACCTTCTGCTGGAAGACCAAGGCTTCACAGAGATGATTC 1594
 DB 2460 CTAACCTTGGATCTGGAACCTTCTGCTGGAAGACCAAGGCTTCACAGAGATGATTC 2519
 QY 1595 TTAGAAGAACTTCTCTGCGCAATAGCAACCTCAGAGTTTACATCATCTGACACCTT 1654
 DB 2520 TTAGAAGAACTTCTCTGCGCAATAGCAACCTCAGAGTTTACATCATCTGACACCTT 2579
 QY 1655 CTCAAAGATATCGTGTAGAGATTGTTAGCATCTACCATTAACCTTCCACACTT 1714
 DB 2580 CTCAAAGATATCGTGTAGAGATTGTTAGCATCTACCATTAACCTTCCACACTT 2639
 QY 1715 CCATCGACGGAAGGCTATCAATCAGGATTAACCTTCGCAACCATGTCAGCGGACAGA 1774
 DB 2640 CCATCGACGGAAGGCTATCAATCAGGATTAACCTTCGCAACCATGTCAGCGGACAGA 2699
 QY 1775 ACTTGCAATCCGAGGCTTCAGAAACGTCGGTTTCACTACTCTTCAACTTCTTAAG 1834
 DB 2700 ACTTGCAATCCGAGGCTTCAGAAACGTCGGTTTCACTACTCTTCAACTTCTTAAG 2759
 QY 1835 GATCAAGGTTTTCACCTTACGCTCATATGTTCAATTTCTGGGAATGAATGATGATG 1894
 DB 2760 GATCAAGGTTTTCACCTTACGCTCATATGTTCAATTTCTGGGAATGAATGATGATG 2819
 QY 1895 ACCGATATGATTTGTGCTCCGAAAGTTACCTTCAGAGCTGAGTACTGAAATTCATGC 1954
 DB 2820 ACCGATATGATTTGTGCTCCGAAAGTTACCTTCAGAGCTGAGTACTGAAATTCATGC 2879
 QY 1955 T 1955
 DB 2880 T 2880

RESULT 11
AAF89825
ID AAF89825 standard; DNA; 7378 BP.
XX
AC AAF89825;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pZ01502.
XX
KW Maize; inbred line R660H; 35S constitutive promoter; Cry1Ab protein;
KW alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome 8;
KW Z1B3; UMC150a; Lepidoptera; Glutofosinate; sweet corn; fungal toxin; ds.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1022..2869
FT /*tag= a
FT /product= "Cry1Ab; encodes AAB83922"
FT CDS 4294..4845
FT /*tag= b
FT /product= "Pat gene; encodes AAB83923"
XX
PN US6232533-B1.
XX
PD 15-MAY-2001.
XX
PF 09-JUN-1999; 99US-0328473.
XX
PR 14-MAR-1997; 97US-0109808.
PR 13-MAR-1998; 98US-0042426.
XX
PA (NOVS) NOVARTIS AG.
P1 Mettler IJ, Plaisted DC, Griener SL, Houghton W, Gardiner M;
XX
XX WPI; 2001-335091/35.
DR P-PSDB; AAB83922, AAB83923.
XX
PT Novel seed of maize inbred line R372H, useful for producing inbred
PT maize plants which on crossing with other different maize plants
PT produce hybrid maize seeds and plants having resistance to insects and
PT herbicide
XX
PS Example 1; Column 21-28; 29pp; English.
XX
XX The specification describes seed and plants of maize inbred line R660H.
CC The seed comprises two cassettes. The first cassette comprises a
CC cauliflower mosaic virus (CaMV) 35S constitutive promoter operably linked
CC to a maize alcohol dehydrogenase intron, a DNA sequence of a gene
CC encoding a Cry1Ab protein, and a terminator functional in plants. The
CC second cassette comprises a CaMV 35S promoter which functions in plant
CC cells operably linked to a maize alcohol dehydrogenase intron, a DNA
CC sequence of a gene encoding for phosphinothricin acetyl transferase, and
CC a terminator functional in plant. The two cassettes are transcribed in
CC the same direction and the nucleic acid construct is incorporated into
CC the seed's genome on chromosome 8 and near position 117, between markers
CC Z1B3 and UMC150a. The maize plants and seeds exhibit resistance to
CC Lepidopteran insects since they express the protein Cry1Ab in high
CC levels, and also exhibit resistance to non-selective herbicide
CC glufosinate. The transgenic maize is suited for preparation of food
CC materials for human or animal consumption e.g. sweet corn for packaging
CC or fresh use as a human food, or grain or silage made from field corn,
CC containing reduced levels of fungal toxins. The present sequence
CC represents plasmid pZ01502, which is used to produce transgenic maize
CC of the invention.
XX
SQ Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other;

Query Match 66.3%; Score 1848.2; DB 22; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;									
QY	95	CCATGGAACAACCCAAACATCAACGAATGCAATTCATACACTGCTTGATACCCAG	154						
DB	1020	CCATGGAACAACCCAAACATCAACGAATGCAATTCATACACTGCTTGATACCCAG	1079						
QY	155	AAGTTGAAGTACTTGGTGAAGAACGATTGAAACCGGTTACATCCATGACATCTCT	214						
DB	1080	AAGTTGAAGTACTTGGTGAAGAACGATTGAAACCGGTTACATCCATGACATCTCT	1139						
QY	215	TGTCCTTGACACAGTTTCTGCTACAGAGTTCCGAGGTCGGGTTGCTTCGGAC	274						
DB	1140	TGTCCTTGACACAGTTTCTGCTACAGAGTTCCGAGGTTGCTTCGGAC	1139						
QY	275	TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGATGCAATTCCTGGTGC	334						
DB	1200	TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGATGCAATTCCTGGTGC	1259						
QY	335	TTGAGCAGTTGATTAACCAAGAGATCGAAGATTCCGACAGAACCCATCTTAGT	394						
DB	1260	TTGAGCAGTTGATTAACCAAGAGATCGAAGATTCCGACAGAACCCATCTTAGT	1319						
QY	395	TGGAAGATTGAGCAATCTCTACCAAAATCTATGACAGAGAGCTGAGAGTGGAGCCG	454						
DB	1320	TGGAAGATTGAGCAATCTCTACCAAAATCTATGACAGAGAGCTTGAAGATGGAGCCG	1379						
QY	455	ATCCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCATTCAGACATGAACAGCG	514						
DB	1380	ATCCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCATTCAGACATGAACAGCG	1439						
QY	515	CTTTGACCAACGCTATCCCATTTGTTCCGAGTCCGAACTACCAAGTCTCTTCTGCG	574						
DB	1440	CTTTGACCAACGCTATCCCATTTGTTCCGAGTCCGAACTACCAAGTCTCTTCTGCG	1499						
QY	575	TGTAGTTCAAGCAGCTAATCTTCAACCTGACGCGCTTCGAGAGTTAGGCTTTGGCG	634						
DB	1500	TGTAGTTCAAGCAGCTAATCTTCAACCTGACGCGCTTCGAGAGTTAGGCTTTGGCG	1559						
QY	635	AAAGTGGGGAATTCATGCTGCAACCAATCAATAGCCGTTTACACGACCTTACTAGCTGA	694						
DB	1560	AAAGTGGGGAATTCATGCTGCAACCAATCAATAGCCGTTTACACGACCTTACTAGCTGA	1619						
QY	695	TTGAAATACACCGACCAACGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	754						
DB	1620	TTGAAATACACCGACCAACGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1679						
QY	755	GTCCGTATTCAGAGATTGATTTAGTACACAGCTTACAGAGAGATTGACCCCTACAG	814						
DB	1680	GTCCGTATTCAGAGATTGATTTAGTACACAGCTTACAGAGAGATTGACCCCTACAG	1739						
QY	815	TTTTGACATTTGTTCTCTCTTCCGAACTATGACTCCGAAACCTTACCTGCTACAG	874						
DB	1740	TTTTGACATTTGTTCTCTCTTCCGAACTATGACTCCGAAACCTTACCTGCTACAG	1799						
QY	875	TGTCCCAACTTACAGAGAAATCTATTAACCAACGATCTTGAACCTTGAACGTTACT	934						
DB	1800	TGTCCCAACTTACAGAGAAATCTATTAACCAACGATCTTGAACCTTGAACGTTACT	1859						
QY	935	TCCGTGTTTGCACCAAGTATTCGAAGGCTCCATCAGGAGCCCACTTGTGACATCT	994						
DB	1860	TCCGTGTTTGCACCAAGTATTCGAAGGCTCCATCAGGAGCCCACTTGTGACATCT	1919						
QY	995	TGAACAGCATTAATTAACCAACGATGCTCAAGAGAGAGATTTACTGTTGACACCC	1054						
DB	1920	TGAACAGCATTAATTAACCAACGATGCTCAAGAGAGAGATTTACTGTTGACACCC	1979						
QY	1055	AGATCATGCTCTTCCCAATGATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1114						
DB	1980	AGATCATGCTCTTCCCAATGATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2039						
QY	1115	CTATGGAACAGCGGCTCCACAAACGATATGTTGCTCAACTAGAGTGTGCTACTA	1174						
DB	2040	CTATGGAACAGCGGCTCCACAAACGATATGTTGCTCAACTAGAGTGTGCTACTA	2099						

QY 1175 GAACCTGTCCTTCCACCTTGTACAGAGAGACCTTCAATATCGTATCAACACGACGAC 1234
 DB 2100 GAACCTGTCCTTCCACCTTGTACAGAGAGACCTTCAATATCGTATCAACACGACGAC 2159
 QY 1335 TTTCCGTTCTTGAGGGAACAGAGTTCCGCTTATGGAACCTCTTCACTTGGCATCCGCTG 1294
 DB 2160 TTTCCGTTCTTGAGGGAACAGAGTTCCGCTTATGGAACCTCTTCACTTGGCATCCGCTG 2219
 QY 1295 TTTACAGAAAGAGCGGAACCGTGTATCTTGGACGAATCCCAACAGAAACAATG 1354
 DB 2220 TTTACAGAAAGAGCGGAACCGTGTATCTTGGACGAATCCCAACAGAAACAATG 2279
 QY 1355 TGCCAGCCGAGCAAGAGATTTCTCCACAGATTGAGCAGTGTCCATGTTCCGTTCCGAT 1414
 DB 2280 TGCCAGCCGAGCAAGAGATTTCTCCACAGATTGAGCAGTGTCCATGTTCCGTTCCGAT 2339
 QY 1415 TCAGCAACAGTTCCGTTGAGCATCATCAGAGCTCCTATGTTCTCATGATTCATGTAATG 1474
 DB 2340 TCAGCAACAGTTCCGTTGAGCATCATCAGAGCTCCTATGTTCTCATGATTCATGTAATG 2399
 QY 1475 CTGAGTTCAACATATCATCTTCTCTCAATATGCAATCCCAATCCATTGACCAAGCTA 1534
 DB 2400 CTGAGTTCAACATATCATCTTCTCTCAATATGCAATCCCAATCCATTGACCAAGCTA 2459
 QY 1535 CTAACTTGTGATCTGGAACCTTCTGTCGTGAAAGAGACAGGCTTCACAGAGGTTGATTTT 1594
 DB 2460 CTAACTTGTGATCTGGAACCTTCTGTCGTGAAAGAGACAGGCTTCACAGAGGTTGATTTT 2519
 QY 1595 TTAGAAGAACTTCTCTGCGCAAGATTAGCAACCTTCAGAGTTTAACTCACTGACCACTTT 1654
 DB 2520 TTAGAAGAACTTCTCTGCGCAAGATTAGCAACCTTCAGAGTTTAACTCACTGACCACTTT 2579
 QY 1655 CTCAAGATATCGTGTGAGAGTTGTTGATGCACTCAACATTAATGAAATTCACACCT 1714
 DB 2680 CTCAAGATATCGTGTGAGAGTTGTTGATGCACTCAACATTAATGAAATTCACACCT 2639
 QY 1715 CCATGACGGAAGGCTTATCATATCAGGTTAACTTCTCCGCAACATGTCAGCGGACCA 1774
 DB 2640 CCATGACGGAAGGCTTATCATATCAGGTTAACTTCTCCGCAACATGTCAGCGGACCA 2699
 QY 1775 ACTTGCAATCCGCGACGCTTCAGAACCGTGGTTTCACTACTCTTCACTTCTTAACG 1834
 DB 2700 ACTTGCAATCCGCGACGCTTCAGAACCGTGGTTTCACTACTCTTCACTTCTTAACG 2759
 QY 1835 GATCAAGGTTTTCACCCCTAGCGCTCATGTTGAATTCGGAATGAAGTACATTG 1894
 DB 2760 GATCAAGGTTTTCACCCCTAGCGCTCATGTTGAATTCGGAATGAAGTACATTG 2819
 QY 1895 ACCGATTTGAGTTTGTGCTGCGGAGGTTACCTTCGAGGCTGAGTACGAAATTCATGC 1954
 DB 2820 ACCGATTTGAGTTTGTGCTGCGGAGGTTACCTTCGAGGCTGAGTACGAAATTCATGC 2879
 QY 1955 T 1955
 DB 2880 T 2880
 RESULT 12
 AAF89834 ID AAF89834 standard; DNA; 7378 BP.
 AC AAF89834;
 XX 23-JUL-2001 (first entry)
 DT Nucleotide sequence of plasmid pZ01502.
 DE Maize; inbred line R660H; 35S constitutive promoter; CryIAb protein;
 XX alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome 8;
 KW 21B3; UMC150a; Lepidoptera; glufosinate; sweet corn; fungal toxin; ds.
 XX Synthetic.
 OS

OS Bacillus thuringiensis.
 XX Key Location/Qualifiers
 FH CDS 1022..2869
 FT CDS /-tag= a
 FT CDS /product= "CryIAb; encodes AAB83924"
 FT CDS 4294..4845
 FT CDS /-tag= b
 FT CDS /product= "Pat gene; encodes AAB83925"
 XX US6232534-B1.
 XX 15-MAY-2001.
 PD 11-JUN-1999; 99US-0330737.
 XX 14-MAR-1997; 97US-0818573.
 PR 13-MAR-1998; 98US-0042426.
 XX (NOVS) NOVARTIS AG.
 PA Mettler IU, Plaisted DC, Grier SL, Houghton W, Gardiner M;
 PI WPI: 2001-335092/35.
 XX P-PSDB; AAB83924, AAB83925.
 DR Novel seed of maize inbred line R660H, useful for producing inbred
 PT maize plants which on crossing with other different maize plants
 PT produce hybrid maize seeds and plants having resistance to insects and
 PT herbicide -
 FT
 PS Example 1; Column 23-32; 24pp; English.
 XX The specification describes seed and plants of maize inbred line R660H.
 CC The seed comprises two cassettes. The first cassette comprises a
 CC cauliflower mosaic virus (CaMV) 35S constitutive promoter operably linked
 CC to a maize alcohol dehydrogenase intron, a DNA sequence of a gene
 CC encoding a CryIAb protein, and a terminator functional in plants. The
 CC second cassette comprises a CamV 35S promoter which functions in plant
 CC cells operably linked to a maize alcohol dehydrogenase intron, a DNA
 CC sequence of a gene encoding for phosphinothricin acetyl transferase, and
 CC a terminator functional in plant. The two cassettes are transcribed in
 CC the same direction and the nucleic acid construct is incorporated into
 CC the seed's genome on chromosome 8 and near position 117, between markers
 CC 21B3 and UMC150a. The maize plants and seeds exhibit resistance to
 CC lepidopteran insects since they express the protein CryIAb in high
 CC levels, and also exhibit resistance to non-selective herbicide
 CC glufosinate. The transgenic maize is suited for preparation of food
 CC materials for human or animal consumption e.g. sweet corn for packaging
 CC or fresh use as a human food, or grain or silage made from field corn,
 CC containing reduced levels of fungal toxins. The present sequence
 CC represents plasmid pZ01502, which is used to produce transgenic maize
 CC of the invention.
 CC
 XX Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other;
 SQ
 Query Match 66.3%; Score 1848.2; DB 22; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 95 CCATGACACAAACCCAAACATCAACGAATGATTCCTATACACTGCTTGAATACCCAG 154
 DB 1020 CCATGACACAAACCCAAACATCAACGAATGATTCCTATACACTGCTTGAATACCCAG 1079
 QY 155 AAGTTGAGATCTTGTGAGAGAGCATTTGAAACCGGTTTACACTCCATCGACATCTCT 214
 DB 1080 AAGTTGAGATCTTGTGAGAGAGCATTTGAAACCGGTTTACACTCCATCGACATCTCT 1139
 QY 215 TGTCTTGAACAGATTTTGTCTCAGCGAGTTGTGTCAGAGTGTGCTGTTCTTGAC 274
 DB 1140 TGTCTTGAACAGATTTTGTCTCAGCGAGTTGTGTCAGAGTGTGCTGTTCTTGAC 1199
 QY 275 TAGTTGACATCATCTGGGATATCTTGTGTCATCTCAATGGAGTGCATTTCTGTGCAAA 334

Db 1200 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGTGCATCTCTGGTGCATA 1259
 Qy 335 TTGAGAGTTGATCAACGAGAGATTCGAAGAGTTCCGCGAGAACGAGCCATCTAGT 394
 Db 1260 TTGAGAGTTGATCAACGAGAGATTCGAAGAGTTCCGCGAGAACGAGCCATCTAGT 1319
 Qy 395 TGAAGAGTTGAGCAATCTCAACCAATCTATGAGAGAGCTTCAGAGAGTGGAAAGCCG 454
 Db 1320 TGAAGAGTTGAGCAATCTCAACCAATCTATGAGAGAGCTTCAGAGAGTGGAAAGCCG 1379
 Qy 455 ATCTTACTAACCCAGCTCTCCGCGAGAAATGCGTATTCATTAACAAGACATGAACAGCG 514
 Db 1380 ATCTTACTAACCCAGCTCTCCGCGAGAAATGCGTATTCATTAACAAGACATGAACAGCG 1439
 Qy 515 CCTTGACACAGCATCTCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTCTGTGCG 574
 Db 1440 CCTTGACACAGCATCTCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTCTGTGCG 1499
 Qy 575 TGTACGTTCAAGCAGCTAATCTTCACTCAGCGTGCCTTCAGACGTTAGCGTGTGGGC 634
 Db 1500 TGTACGTTCAAGCAGCTAATCTTCACTCAGCGTGCCTTCAGACGTTAGCGTGTGGGC 1559
 Qy 635 AAAAGTGGGAGTTGCATGCTCGACACATCAATAGCCGTTTACAAGACCTTACTAGGCTGA 694
 Db 1560 AAAAGTGGGAGTTGCATGCTCGACACATCAATAGCCGTTTACAAGACCTTACTAGGCTGA 1619
 Qy 695 TTGAAAATTACACCGACCGCTGTTGTTGGTGTACAACTAGGCTTGGAGCGTGTGCG 754
 Db 1620 TTGAAAATTACACCGACCGCTGTTGTTGGTGTACAACTAGGCTTGGAGCGTGTGCG 1679
 Qy 755 GTCTGATTTAGAGATTGATTAGATACAAACAGTTGAGAGAGAAATGACCTCAGAC 814
 Db 1680 GTCTGATTTAGAGATTGATTAGATACAAACAGTTGAGAGAGAAATGACCTCAGAC 1739
 Qy 815 TTTTGAATTTGTGTCTCTCTCCGAACTATGATCCAGAACCTTACCTTACCTGATACG 874
 Db 1740 TTTTGAATTTGTGTCTCTCTCCGAACTATGATCCAGAACCTTACCTTACCTGATACG 1799
 Qy 875 TGTCCCACTTACCGAGAAATCTATACTAACCCAGTTCTTGAGAACTTCGACGCTAGCT 934
 Db 1800 TGTCCCACTTACCGAGAAATCTATACTAACCCAGTTCTTGAGAACTTCGACGCTAGCT 1859
 Qy 935 TCCGTGTTCTGCCCCAGGATTCGAAGGCTCCATCAGAGAGCCACACTTGATGACATCT 994
 Db 1860 TCCGTGTTCTGCCCCAGGATTCGAAGGCTCCATCAGAGAGCCACACTTGATGACATCT 1919
 Qy 995 TGAACAGCATTAATCTATCAACCGATGCTCACAGAGAGATTAATGCTGTCGACACC 1054
 Db 1920 TGAACAGCATTAATCTATCAACCGATGCTCACAGAGAGATTAATGCTGTCGACACC 1979
 Qy 1055 AGATCATGGCCTCTCAGTTGAGATTCAAGCGGCGGAGTTTACCTTCTCTCTATGGA 1114
 Db 1980 AGATCATGGCCTCTCAGTTGAGATTCAAGCGGCGGAGTTTACCTTCTCTCTATGGA 2039
 Qy 1115 CTATGGAAGAACGCGCTCCACAACAACGATGTTGCTCACTAGGTCAGGCTGTCTACA 1174
 Db 2040 CTATGGAAGAACGCGCTCCACAACAACGATGTTGCTCACTAGGTCAGGCTGTCTACA 2099
 Qy 1175 GAACCTTGTCTCCACTTTGTACAGAAAGCCCTTCAATATCGGTATCAACAACGAGAC 1234
 Db 2100 GAACCTTGTCTCCACTTTGTACAGAAAGCCCTTCAATATCGGTATCAACAACGAGAC 2159
 Qy 1235 TTTCCGTTCTTGACGGAACAGAGTTGCTATGAAACCTTCTAATCTTGCCATCGCGTG 1294
 Db 2160 TTTCCGTTCTTGACGGAACAGAGTTGCTATGAAACCTTCTAATCTTGCCATCGCGTG 2219
 Qy 1295 TTTACAGAAAGACGGAACGTTGATTCCTTGACGAAATCCACACAGAACCAACATG 1354
 Db 2220 TTTACAGAAAGACGGAACGTTGATTCCTTGACGAAATCCACACAGAACCAACATG 2279
 Qy 1355 TGCACCCGAGCAAGATTCCTCCACAGTTGAGCCAGTGTCAATGTTCCGTTCCGAT 1414

Db 2280 TGCCACCCAGCAAGGATTCCTCCACAGTTGAGCACAGTGTCCATGTTCCGTTCCGAT 2339
 Qy 1415 TCAGCAACAGTTCCTGAGACATCATCAGAGCTCTATGTTCTCATGATTCATGATG 1474
 Db 2240 TCAGCAACAGTTCCTGAGACATCATCAGAGCTCTATGTTCTCATGATTCATGATG 2399
 Qy 1475 CTGATTCACAAATATCATTTCTTCTCTCTCAATTCACCCAAATCCCATTTGACCAAGTCTA 1534
 Db 2400 CTGATTCACAAATATCATTTCTTCTCTCTCAATTCACCCAAATCCCATTTGACCAAGTCTA 2459
 Qy 1535 CTACCTTGTATCGGAACCTTCTGTGTGAAGAGCCAGGCTTCACAGAGGTATATTC 1594
 Db 2460 CTACCTTGTATCGGAACCTTCTGTGTGAAGAGCCAGGCTTCACAGAGGTATATTC 2519
 Qy 1595 TTAGAGAACTTCTCTGCGCAGATTAGACACCTCAGAGTTTACATCATCAGACACTTT 1654
 Db 2520 TTAGAGAACTTCTCTGCGCAGATTAGACACCTCAGAGTTTACATCATCAGACACTTT 2579
 Qy 1655 CTCAAAATATCGTGTAGAGATTGCTTACGATCTACCACTTACTTTCACACCT 1714
 Db 2580 CTCAAAATATCGTGTAGAGATTGCTTACGATCTACCACTTACTTTCACACCT 2639
 Qy 1715 CCATGACGGAAGGCTTATCAATCAGGATTAATCTCCGCAACCATGTCAGGCGACGA 1774
 Db 2640 CCATGACGGAAGGCTTATCAATCAGGATTAATCTCCGCAACCATGTCAGGCGACGA 2699
 Qy 1775 ACTTGCAATCCGGAAGCTTCAGAACCGTGGTTCATCTCTTCAACTTCTTAAAG 1834
 Db 2700 ACTTGCAATCCGGAAGCTTCAGAACCGTGGTTCATCTCTTCAACTTCTTAAAG 2759
 Qy 1835 GATCAAGGCTTTTACCTTACCTTACGCTCATGTTTCAATTTGCGCAATGAATGATGATG 1894
 Db 2760 GATCAAGGCTTTTACCTTACCTTACGCTCATGTTTCAATTTGCGCAATGAATGATGATG 2819
 Qy 1895 ACCGATATGATTTGTGCTGCTCCGAAAGTTACCTTCAGAGCTGAGTACTGAAATTCATGC 1954
 Db 2820 ACCGATATGATTTGTGCTGCTCCGAAAGTTACCTTCAGAGCTGAGTACTGAAATTCATGC 2879
 Qy 1955 T 1955
 Db 2880 T 2880

RESULT 13
 ABL57440
 ID ABL57440 standard; DNA; 7378 BP.
 XX
 AC ABL57440;
 XX
 DT 12-AUG-2002 (first entry)
 XX
 DE Plasmid pZ01502 encoding insect and herbicide resistance in maize.
 XX
 DE Maize; crop improvement; transgenic plant; disease resistance;
 XX insect resistance; herbicide resistance; pZ01502; ds.
 KM
 OS Chimeric - Zea mays.
 OS Chimeric - Cauliflower mosaic virus.
 OS Chimeric - Streptomyces sp.
 OS Chimeric - Bacillus thuringiensis kurstaki.
 XX
 PN US6129575-B1.
 XX
 PD 11-DEC-2001.
 XX
 PF 09-JUN-1999; 99US-0329169.
 XX
 PR 14-MAR-1997; 97US-109808P.
 PR 13-MAR-1998; 98US-0042426.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Mettler ID, Mies D:

XX WPI: 2002-121141/16.
 DR New maize inbred line 2227BT, ATCC 203942, useful for animal and human
 XX nutrition, contains genes for resistance to insects and herbicide
 PT
 XX Example 1: Column 25-32; 24bp; English.
 XX
 CC The present sequence is the nucleotide sequence of plasmid pZ01502
 CC (ATCC 209682). The plasmid includes an expression cassette for
 CC *Bacillus thuringiensis* kurstaki CryIAb crystal protein and an
 CC expression cassette for phosphinothricin acetyltransferase (see
 CC also ABL57432-39). Seed of maize inbred line 2227BT (ATCC 203942)
 CC is claimed, which comprises a nucleic acid construct comprising
 CC these 2 expression cassettes transcribed in the same direction and
 CC incorporated into the seed's genome on chromosome 8, near position
 CC 117, between markers Z1B3 and UMC150a. Also claimed are a maize
 CC plant of inbred line 2227BT, its pollen, ovules and other plant
 CC parts, as well as hybrid seed produced by crossing the plant with
 CC an inbred maize plant of different genotype. The nucleic acid
 CC construct imparts resistance to phosphinothricin (glyphosate)
 CC herbicide and to insects, particularly European corn borer
 CC (*Ostrinia nubilalis*). Southwestern corn borer (*Diatraea grandiosella*)
 CC and Fall armyworm (*Spodoptera frugiperda*). Grain and silage
 CC produced from the new plants have reduced contents of aflatoxin,
 CC possibly because the insect resistance provided by CryIAb reduces
 CC opportunistic fungal infections.
 CC
 XX Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other:
 50
 Query Match 66.3%; Score 1848.2; DB 24; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 695 TTGAAACCTACACCGACCGCTGTTGGTATCAACACTGCTGGAGCTGTGG 754
 |||||
 DB 1620 TTGAAACCTACACCGACCGCTGTTGGTATCAACACTGCTGGAGCTGTGG 1679
 QY 755 GTCTGATTTCTAGAGATTGATATGATCAACAGCTTCAGAGAGATTACCTCAG 814
 |||||
 DB 1680 GTCTGATTTCTAGAGATTGATATGATCAACAGCTTCAGAGAGATTACCTCAG 1739
 QY 815 TTTTGACATTGTGTCTCTCTCCCGAAGTATGACTCCAACTACCTATCCGTACAG 874
 |||||
 DB 1740 TTTTGACATTGTGTCTCTCTCCCGAAGTATGACTCCAACTACCTATCCGTACAG 1799
 QY 875 TGTCCCACTTACCAAGAAATCTATACCACTGTTCTTGAGACTTGCACGGTACT 934
 |||||
 DB 1800 TGTCCCACTTACCAAGAAATCTATACCACTGTTCTTGAGACTTGCACGGTACT 1859
 QY 935 TCCGTGTTCTGCCAAGGTATGGAAGGCTCCATCAGAGGCCACCTGATGAGCATCT 994
 |||||
 DB 1860 TCCGTGTTCTGCCAAGGTATGGAAGGCTCCATCAGAGGCCACCTGATGAGCATCT 1919
 QY 995 TGAACACATTAATCTATACACCGATGCTCAGAGAGAGATTTACTGTGTGAGACCC 1054
 |||||
 DB 1920 TGAACACATTAATCTATACACCGATGCTCAGAGAGAGATTTACTGTGTGAGACCC 1979
 QY 1055 AGATCATGCTCTCCAGTTGATTCAGCGGGCCGAGTTTACTCTCTATGAA 1114
 |||||
 DB 1980 AGATCATGCTCTCCAGTTGATTCAGCGGGCCGAGTTTACTCTCTATGAA 2039
 QY 1115 CTATGGGAAAGCGCGCTCCACAAACAGTATCGTTGCTCAACTGATGATGATGATCA 1174
 |||||
 DB 2040 CTATGGGAAAGCGCGCTCCACAAACAGTATCGTTGCTCAACTGATGATGATGATCA 2099
 QY 1175 GAACCTTGTTCCACCTGATCAGAGAGACCTTCAATATGATGATCAACACAGCAAC 1234
 |||||
 DB 2100 GAACCTTGTTCCACCTGATCAGAGAGACCTTCAATATGATGATCAACACAGCAAC 2159
 QY 1235 TTTTCGTTCTTGACGGAACAGAGTTGCTATGGAACCTCTTCTTACTGTCATCCGCTG 1294
 |||||
 DB 2160 TTTTCGTTCTTGACGGAACAGAGTTGCTATGGAACCTCTTCTTACTGTCATCCGCTG 2219
 QY 1295 TTTTACAAAGAGGGAACCGTTGATTCCTTGAGAGAAATCCCAACAGAAACAATG 1354
 |||||
 DB 2220 TTTTACAAAGAGGGAACCGTTGATTCCTTGAGAGAAATCCCAACAGAAACAATG 2279
 QY 1355 TGCCACCGAGCAAGATTTCTCCACAGTTGAGCCAGTGCATGTTCCGTTCCGAT 1414
 |||||
 DB 2280 TGCCACCGAGCAAGATTTCTCCACAGTTGAGCCAGTGCATGTTCCGTTCCGAT 2339
 QY 1415 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTTATGTTCTATGATTCATGTAAGT 1474
 |||||
 DB 2340 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTTATGTTCTATGATTCATGTAAGT 2399
 QY 1475 CTGAGTTCAAAATATCATTTCTCTCTCAAAATCACCAGAAATCCCAATGCAAGTCTA 1534
 |||||
 DB 2400 CTGAGTTCAAAATATCATTTCTCTCTCAAAATCACCAGAAATCCCAATGCAAGTCTA 2459
 QY 1535 CTAACCTTGATCTGGAATCTCTGCTGGAAGACAGGCTTCAAGAGAGTATATTC 1594
 |||||
 DB 2460 CTAACCTTGATCTGGAATCTCTGCTGGAAGACAGGCTTCAAGAGAGTATATTC 2519
 QY 1595 TTAGAAGAACTTCTCTGCGCAAGTATGACACCTCTCAGATTAATCATCTGCAACCTTT 1654
 |||||
 DB 2520 TTAGAAGAACTTCTCTGCGCAAGTATGACACCTCTCAGATTAATCATCTGCAACCTTT 2579
 QY 1655 CTCAAGATATCGTGCAGATTGGTTAGCATACCACTTAATGCAATTCGCACTCT 1714
 |||||
 DB 2580 CTCAAGATATCGTGCAGATTGGTTAGCATACCACTTAATGCAATTCGCACTCT 2639
 QY 1715 CCATGACGGAAGGCTATATCAATCAGGGTAACTTCTCCGCAACCATGTCAGCGGACAGA 1774
 |||||
 DB 2640 CCATGACGGAAGGCTATATCAATCAGGGTAACTTCTCCGCAACCATGTCAGCGGACAGA 2699

Oy	1775	ACTTGCATATCCGGAGCGATTTGAGAACCCGTCGGTTTACTACTCTCTTCAACTTCTTAACG	1835
Db	2700	ACTTGCAATCCGGAGCGATTTGAGAACCCGTCGGTTTACTACTCTCTTCAACTTCTTAACG	2755
Oy	1835	GATCAAGCGTTTACCCCTTAGCCGCTCAGTGTTCATTTCTGGCAATGAGTACATTG	1894
Db	2760	GATCAAGCGTTTACCCCTTAGCCGCTCAGTGTTCATTTCTGGCAATGAGTACATTG	2819
Oy	1895	ACCGTATTGAGTTTGTGCTGCTGCGAAGTTACCTTGGAGCTGAGTACTAGAAATTCATGC	1954
Db	2820	ACCGTATTGAGTTTGTGCTGCTGCGAAGTTACCTTGGAGCTGAGTACTAGAAATTCATGC	2875
Oy	1955	T 1955	
Db	2880	T 2880	
RESULT 14			
ID	AAA75460	AAA75460 standard; DNA; 1851 BP.	
AC	AAA75460;		
XX			
DT	15-JAN-2001	(first entry)	
DE			
XX			
XX			
KW	35S promoter; alcohol dehydrogenase intron; nopaline synthase terminator;		
KW	insecticidal Cry IAb protein toxin; transgenic plant; fungal toxin;		
KW	afلاتoxin; baculovirus; Lepidopteran insect; glutosinate; ds.		
XX			
OS	Synthetic.		
XX	Bacillus thuringiensis.		
FH	Key	Location/Qualifiers	
FT	CDS	2..1849	
FT		/*tag= a	
FT		/product= "Cry IAb"	
XX			
PN	US6114608-A.		
XX			
PD	05-SEP-2000.		
XX			
PF	13-MAR-1998;	98US-0042426.	
XX			
PR	14-MAR-1997;	97US-0109808.	
XX			
PA	(NOVS) NOVARTIS AG.		
XX			
PI	Dietrich PS, Mettler JF, Sinibaldi RM;		
XX			
DR	WPI: 2000-586487/55.		
XX	P-PSDB; AAB18416.		
PT			
PT	Novel DNA construct comprising an expression cassette having a		
XX	functional constitutive promoter, operably linked to a maize alcohol		
PT	dehydrogenase intron, gene encoding Cry IAb protein and a terminator		
XX			
XX	Claim 1; Column 19-22; 24pp; English.		
PS			
XX			
CC	The present sequence encodes a Cry IAb toxin, which is used to create		
CC	the construct of the invention. The specification describes a nucleic		
CC	acid construct, comprising an expression cassette containing a		
CC	cauliflower mosaic virus (CaMV) 35S promoter, a maize alcohol		
CC	dehydrogenase intron, a DNA molecule encoding an insecticidal Cry IAb		
CC	protein toxin and a NOS (nopaline synthase) terminator in operable		
CC	linkage. The nucleic acid constructs are useful for producing transgenic		
CC	plants such as maize, wheat, barley, sorghum and rice. Preferably, maize		
CC	plants such as field corn, sweet corn, white corn, silage corn or popcorn		
CC	are produced. The transgenic maize is used for preparing food materials		
CC	with reduced levels of fungal toxins, e.g. aflatoxins. The transgenic		
CC	plants express a baculovirus crystal protein toxin, which is effective		
CC	against lepidopteran insects at relatively high levels and further		
CC	against lepidopteran insects at relatively high levels and further		

CC	XX	Seq	Sequence	1851 BP; 478 A; 504 C; 394 G; 475 T; 0 other;	66.2%: Score 1845.4; DB 21; Length 1851; Best Local Similarity 99.9%; Pred. No. 0; Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC			provides resistance to the non-selective herbicide glufosinate.		
QY		96	CATGAGACAAACCCAAACATCAAGATGATTCATACACTGCTTGAATACCCAGA	155	
Db		1	CATGAGACAAACCCAAACATCAAGATGATTCATACACTGCTTGAATACCCAGA	60	
QY		156	AGTTGAAGTACTTGTGTGAGAACGCAATTGAAACCGGTACACTCCCATCGACATCTCTT	215	
Db		61	AGTTGAAGTACTTGTGTGAGAACGCAATTGAAACCGGTACACTCCCATCGACATCTCTT	120	
QY		216	GTCCTTACACAGTTTCGCTCAGCGAGTTCTGTCACAGGTCGTGGGTTCGTTCTCGGACT	275	
Db		121	GTCCTTACACAGTTTCGCTCAGCGAGTTCTGTCACAGGTCGTGGGTTCGTTCTCGGACT	180	
QY		276	AGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGTGCATTTCTGTGCAAT	335	
Db		181	AGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGTGCATTTCTGTGCAAT	240	
QY		336	TGACAGTGTGATCAACCAAGAGATCGAAGATTCCGACAGAACCAAGGCATCTTAGTT	395	
Db		241	TGACAGTGTGATCAACCAAGAGATCGAAGATTCCGACAGAACCAAGGCATCTTAGTT	300	
QY		396	GGAAGGATGAGCAATCTTACCAAACTATGACAGAGCTTCAGAGAGTGGGAAGCGCA	455	
Db		301	GGAAGGATGAGCAATCTTACCAAACTATGACAGAGCTTCAGAGAGTGGGAAGCGCA	360	
QY		456	TCTCTACTAACCCAGCTCTCCGCGAGAGAAATGCGTATTCATTTCAACGACATGAACAGCGC	515	
Db		361	TCTCTACTAACCCAGCTCTCCGCGAGAGAAATGCGTATTCATTTCAACGACATGAACAGCGC	420	
QY		516	CTTGAACACAGCTATTCCTCATTTGTCGAGTCGAGAACTACCAAGTTCTCTTGTCCGT	575	
Db		421	CTTGAACACAGCTATTCCTCATTTGTCGAGTCGAGAACTACCAAGTTCTCTTGTCCGT	480	
QY		576	GTAAGTTACAGACGTAATCTTCACTCAGGTCCTTCGAGACCTTACCGGTTTGGCA	635	
Db		481	GTAAGTTACAGACGTAATCTTCACTCAGGTCCTTCGAGACCTTACCGGTTTGGCA	540	
QY		636	AAGGTGGGGATTCGATGCTGCACATCAATAGCCGTTTCAACAGACCTTACAGGCTGAT	695	
Db		541	AAGGTGGGGATTCGATGCTGCACATCAATAGCCGTTTCAACAGACCTTACAGGCTGAT	600	
QY		696	TGAAACATCACCGACCAACGCTGTTGCTGTGTAGAACACTGGCTTGGAGCGTGTCTGGGG	755	
Db		601	TGAAACATCACCGACCAACGCTGTTGCTGTGTAGAACACTGGCTTGGAGCGTGTCTGGGG	660	
QY		756	TCTGATTTCTGAGATTGAGTTGATTAATACACCAAGTTACAGAGAGAAATTTGACACCTTCACAGT	815	
Db		661	TCTGATTTCTGAGATTGAGTTGATTAATACACCAAGTTACAGAGAGAAATTTGACACCTTCACAGT	720	
QY		816	TTTGGACATGTTGTTCTCTTCCGGAATAGATCCGGAACCTTACCTTACCGTACAGT	875	
Db		721	TTTGGACATGTTGTTCTCTTCCGGAATAGATCCGGAACCTTACCTTACCGTACAGT	780	
QY		876	GTCCCAACTTACAGAGAAATCTTACTAACCCAGTTCTTGAGAACTTTCGACGGTAGCTT	935	
Db		781	GTCCCAACTTACAGAGAAATCTTACTAACCCAGTTCTTGAGAACTTTCGACGGTAGCTT	840	
QY		936	CCGTGTTCTGCCCCAAGATTCGAAGGTCATACAGAGCCCACTTGATGAGACATCTT	995	
Db		841	CCGTGTTCTGCCCCAAGATTCGAAGGTCATACAGAGCCCACTTGATGAGACATCTT	900	
QY		996	GAAACGACATTAATCTATCTACACCGATGCTCAACAGAGAGAGTATTACTGTTGACACCA	1055	
Db		901	GAAACGACATTAATCTATCTACACCGATGCTCAACAGAGAGAGTATTACTGTTGACACCA	960	
QY		1056	GATCATGGCCCTCTCCAGTTGGAATTCAGCGGGCCCGAGTTTACTCTTCTCTATGGAAC	1115	

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Db      961  GATCATGCGCTCTCTCAGTTGGATTACAGGGCCGAGTTTACCTTCTCTCTATGTAAC 1020
Oy      1116  TATGGAAAGCGCGCTCACAACAACGATGTTGCTCACTAGGTGAGGNGTCTACAG 1175
Db      1021  TATGGAAAGCGCGCTCACAACAACGATGTTGCTCACTAGGTGAGGNGTCTACAG 1080
Oy      1176  AACCTTGCTTCCACTTGTACAGAAAGACCTTCAATATCGGTATCAACAACGAACT 1235
Db      1081  AACCTTGCTTCCACTTGTACAGAAAGACCTTCAATATCGGTATCAACAACGAACT 1140
Oy      1236  TTCCGTTCTTACAGGAACAGAGTTGCTGCTATGAAACCTTCTTCAACTTCCGCTGT 1295
Db      1141  TTCCGTTCTTACAGGAACAGAGTTGCTGCTATGAAACCTTCTTCAACTTCCGCTGT 1200
Oy      1296  TTACGAAGAAGCGGAACCGTTGATTCCTTGGAGGAATCCACACAGAAACAACATGT 1355
Db      1201  TTACGAAGAAGCGGAACCGTTGATTCCTTGGAGGAATCCACACAGAAACAACATGT 1260
Oy      1356  GCCACCCAGGAGGATTCCTCCACAGGTTGAGCCAGCTGTCCATGTTCCGTTCCGAT 1415
Db      1261  GCCACCCAGGAGGATTCCTCCACAGGTTGAGCCAGCTGTCCATGTTCCGTTCCGAT 1320
Oy      1416  CAGCAACAGTTCCGTCAGCATCATAGAGCTCTATGTTCTCATGAGATTCACTGTAAGC 1475
Db      1321  CAGCAACAGTTCCGTCAGCATCATAGAGCTCTATGTTCTCATGAGATTCACTGTAAGC 1380
Oy      1476  TGAGTTCAACAATATCATCTCTCTCTCAATACCCCAATCCCATTTGACCAAGTCTAC 1535
Db      1381  TGAGTTCAACAATATCATCTCTCTCTCAATACCCCAATCCCATTTGACCAAGTCTAC 1440
Oy      1536  TAACCTTGATCTGGAACTTCTGTGCTGTAAGAAAGAACAGGCTTACAGAGGTGATATTCT 1595
Db      1441  TAACCTTGATCTGGAACTTCTGTGCTGTAAGAAAGAACAGGCTTACAGAGGTGATATTCT 1500
Oy      1596  TAGAAGAACTTCTCTGCGCAGATTAGACACCTCTCAGATTAAATCATCATGCCACTTTC 1655
Db      1501  TAGAAGAACTTCTCTGCGCAGATTAGACACCTCTCAGATTAAATCATCATGCCACTTTC 1560
Oy      1656  TCMAAGATATGCTGTCAGGATTCGTTAGCATCTCACTCACTTGAATTCCACAGCTC 1715
Db      1561  TCMAAGATATGCTGTCAGGATTCGTTAGCATCTCACTCACTTGAATTCCACAGCTC 1620
Oy      1716  CATGACCGAAGGCTTATCAATCAGAGTTAATCTTCCGAAACATATGTCAGGCGAGCA 1775
Db      1621  CATGACCGAAGGCTTATCAATCAGAGTTAATCTTCCGAAACATATGTCAGGCGAGCA 1680
Oy      1776  CTTCGAATCCGCGAGCTTCAGAACCGTGGCTTCACTACTCTTTCAACTTCTTAAAGG 1835
Db      1681  CTTCGAATCCGCGAGCTTCAGAACCGTGGCTTCACTACTCTTTCAACTTCTTAAAGG 1740
Oy      1836  ATCAGACGTTTTCACCTTAGCGCTCATGTTGTTCAATTTGCAATGGAAGTATACATGA 1895
Db      1741  ATCAGACGTTTTCACCTTAGCGCTCATGTTGTTCAATTTGCAATGGAAGTATACATGA 1800
Oy      1896  CCGTATTTGATTTGCTGCTGCGGAAGTTAATCTTGAAGGCTGAGTACT 1942
Db      1801  CCGTATTTGATTTGCTGCTGCGGAAGTTAATCTTGAAGGCTGAGTACT 1847

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RESULT 15

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AAD06308  AAD06308 standard; DNA; 1851 BP.
XX AC      AAD06308;
XX DE      10-AUG-2001 (first entry)
XX DE      Insecticidal CryIAb toxin DNA of Bt kurstaki expression cassette.
XX DE      Transgenic maize; expression cassette; 35S promoter;
XX DE      alcohol dehydrogenase intron; nopaline synthetase; NOS terminator;
XX DE      crystal IAb; CryIAb toxin; foodstuffs preparation; ds.

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XX OS      Bacillus thuringiensis.
XX FH      Key
XX FT      CDS
XX FT      Location/Qualifiers
XX FT      2..1849
XX FT      /*tag= a
XX FT      /product= "Insecticidal CryIAb toxin"
XX US6222104-B1.
XX PD      24-APR-2001.
XX PF      13-APR-1999; 99US-0291238.
XX PR      09-NOV-1994; 94US-0336627.
XX PR      22-AUG-1996; 96US-0716836.
XX PR      14-MAR-1997; 97US-0818573.
XX PR      13-MAR-1998; 98US-0042426.
XX PA      (NOVS ) NOVARTIS AG.
XX PI      Mettler LJ, Krieger M, Mies D;
XX DR      WPI; 2001-327266/34.
XX DR      P-PSDB; AAE02360.
XX PT      Novel transgenic maize seed for hybrid maize plant production,
XX PT      comprising expression cassette linked operably with CAMV 35S promoter,
XX PT      alcohol dehydrogenase intron, insecticidal CryIAb toxin gene or NOS
XX PT      terminator
XX PS      Claim 1; Column 19-22; 24pp; English.
XX CC      The present invention relates to transgenic maize seed for hybrid maize
XX CC      plant production, comprising an expression cassette linked operably with
XX CC      constitutive Cauliflower mosaic virus (CaMV) 35S promoter, an alcohol
XX CC      dehydrogenase intron, a DNA encoding an insecticidal
XX CC      Bacillus thuringiensis (Bt) CryIAb toxin and a nopaline synthetase (NOS)
XX CC      terminator. The transgenic maize seed is used in maize cultivation
XX CC      methods for propagating hybrid maize seeds and for growing hybrid maize
XX CC      plants. The maize is also used in foodstuffs preparation for animal or
XX CC      human consumption. The inbred maize line NP948 of the invention has
XX CC      reduced level of fungal toxins, hence suitable for foodstuffs
XX CC      preparation. Yield is high. Plant health is improved due to reduced
XX CC      stalk rot. Grain test weight is high and the rate of grain dry down is
XX CC      reduced. The present sequence is insecticidal crystal IAb (CryIAb) toxin
XX CC      DNA of Bt kurstaki expression cassette.
XX SQ      Sequence 1851 BP; 478 A; 504 C; 394 G; 475 T; 0 other;
XX
XX Query Match 66.2%; Score 1845.4; DB 22; Length 1851;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Job time : 713 secs

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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 04:55:27 ; Search time 188 Seconds
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1848.2	66.3	7378	3	US-09-042-426-9 Sequence 9, Appli
2	1848.2	66.3	7378	3	US-09-291-228-9 Sequence 9, Appli
3	1848.2	66.3	7378	3	US-09-330-760-9 Sequence 9, Appli
4	1848.2	66.3	7378	3	US-09-328-473-9 Sequence 9, Appli
5	1848.2	66.3	7378	3	US-09-330-737-9 Sequence 9, Appli
6	1848.2	66.3	7378	4	US-09-329-169-9 Sequence 9, Appli
7	1848.2	66.3	7378	4	US-09-330-714A-9 Sequence 9, Appli
8	1848.2	66.3	7378	4	US-09-328-826-9 Sequence 9, Appli
9	1848.2	66.3	7378	4	US-09-289-170-9 Sequence 9, Appli
10	1848.2	66.3	7378	3	US-09-042-426-3 Sequence 3, Appli
11	1848.2	66.2	1851	3	US-09-291-228-3 Sequence 3, Appli
12	1848.2	66.2	1851	3	US-09-330-760-3 Sequence 3, Appli
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14	1848.2	66.2	1851	3	US-09-330-737-3 Sequence 3, Appli
15	1848.2	66.2	1851	4	US-09-329-169-3 Sequence 3, Appli
16	1848.2	66.2	1851	4	US-09-330-714A-3 Sequence 3, Appli
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18	1848.2	66.2	1851	4	US-09-289-170-3 Sequence 3, Appli
19	1848.2	66.2	1851	2	US-08-841-178-22 Sequence 22, Appl
20	1848.2	66.2	3484	1	US-08-530-492-105 Sequence 105, App
21	1848.2	66.2	3484	1	US-08-906-517-105 Sequence 105, App
22	1848.2	66.1	1845	1	US-07-951-715A-5 Sequence 5, Appli
23	1848.2	66.1	1845	2	US-08-459-448A-5 Sequence 5, Appli
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26	1848.2	66.1	1845	3	US-08-459-444-5 Sequence 5, Appli
27	1848.2	66.1	1845	4	US-09-547-422-5 Sequence 5, Appli

28	1843.4	66.1	3531	1	US-08-530-492-3	Sequence 3, Appli
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38	1220.4	43.8	2815	1	US-07-671-817A-2	Sequence 2, Appli
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40	1220.4	43.8	4014	1	US-08-466-486-1	Sequence 1, Appli
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44	1220.4	43.8	4360	3	US-09-021-203-1	Sequence 1, Appli
45	1220	43.8	3468	1	US-07-951-715A-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-042-426-9
; Sequence 9, Application US/09042426
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6114608artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042.426
; FILING DATE: March 13, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: Complete sequence of pZ01502
; US-09-042-426-9
;
; Query Match 66.3%, Score 1848.2, DB 3, Length 7378;
; Best Local Similarity 99.6%, Pred. No. 0;
; Matches 1853, Conservative 0, Mismatches 8, Indels 0, Gaps 0;
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RESULT 2
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; Sequence 9, Application US/09291238
; Patent No. 6222104
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6222104artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7378 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Complete sequence of pZ01502
US-09-291-238-9

Query March 66.3%; Score 1848.2; DB 3; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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DB 1920 TGAACAGCATTAATCTATCAACCGATGCTCAACAGAGAGATTAATCTGTGAGACACC 1979
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DB 1980 AGATCAGGCTCTCCAGTTGAGATTCAGCGGCGCCGAGTTTACCTTCTCTATGGA 2039
QY 1115 CTATGGAAGAACGCGCTCCCAACACATGATCTGTTGCTCAACTGAGGTGTCTACA 1174
DB 2040 CTATGGAAGAACGCGCTCCCAACACATGATCTGTTGCTCAACTGAGGTGTCTACA 2099
QY 1175 GAACCTTGTCTTCCACTTGTACAGAGACCTTCAATATCGGTATCAACACAGCAAC 1234
DB 2100 GAACCTTGTCTTCCACTTGTACAGAGACCTTCAATATCGGTATCAACACAGCAAC 2159
QY 1235 TTTCCGTTTGAAGGAACAGAGTTGGCTATGGAACCTCTTCACTGTCATCCGCTG 1294
DB 2160 TTTCCGTTTGAAGGAACAGAGTTGGCTATGGAACCTCTTCACTGTCATCCGCTG 2219
QY 1295 TTTACAGAAAGAGGGAACCGTTGATTCCTTGAAGAAATCCCAACAGAAACAATG 1354
DB 2220 TTTACAGAAAGAGGGAACCGTTGATTCCTTGAAGAAATCCCAACAGAAACAATG 2279
QY 1355 TGCCACCGAGCAAGATTTCTCCACAGGTTGAGCCAGTGTCCATGTTCCGTTCCGAT 1414
DB 2280 TGCCACCGAGCAAGATTTCTCCACAGGTTGAGCCAGTGTCCATGTTCCGTTCCGAT 2339
QY 1415 TCAGCAACAGTTCGATGAGATTCATCAGAGCTCTATGTTCTCATGATTCATGTTAGTG 1474
DB 2340 TCAGCAACAGTTCGATGAGATTCATCAGAGCTCTATGTTCTCATGATTCATGTTAGTG 2399
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DB 2460 CTAACTTGGATCTGGAACCTTCTGTGTAAGGAACAGGCTTCAACAGAGAGTATATTC 2519
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DB 2520 TTAGAAGAACTTCTCTGCGGAGATTTAGCACTTCAAGTTTATATATCACTGACACATTT 2579
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DB 2580 CTCAAGATATCTGTGAGATTTGATACGATCTACCACTTGTGCAATTTCAACACT 2639
QY 1715 CCATGACGGAAGGCTATCAATCAGGTTAATCTTCCGCAACATGTCAGCGGACGA 1774
DB 2640 CCATGACGGAAGGCTATCAATCAGGTTAATCTTCCGCAACATGTCAGCGGACGA 2699
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Db 2700 ACTGCAATCCGACGCTTCAAGAACCGTGGTTTCACTACTCTTCACTTCTCTACG 2759
Qy 1835 GATCAAGCGTTTTCACCTTAGCGCTCATGTTCATTTGCGAATGAGATGATACATG 1894
Db 2760 GATCAAGCGTTTTCACCTTAGCGCTCATGTTCATTTGCGAATGAGATGATACATG 2819
Qy 1895 ACCGTAATGAGTTGTGCTCCGGAAGTTACCTTCGAGCTGAGTACTGAGAAATTCATGC 1954
Db 2820 ACCGTAATGAGTTGTGCTCCGGAAGTTACCTTCGAGCTGAGTACTGAGAAATTCATGC 2879
Qy 1955 T 1955
Db 2880 T 2880

RESULT 3
US-09-330-760-9
Sequence 9, Application US/09330760
Patent No. 6229075

GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA

ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7378 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Complete sequence of pZ01502

US-09-330-760-9

Query Match 66.3%; Score 1848.2; DB 3; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 95 CCATGACAAACCAACCAATCAAGATGATTCATCAACATGCTTGAGTAAACCAAG 154
Db 1020 CCATGACAAACCAACCAATCAAGATGATTCATCAACATGCTTGAGTAAACCAAG 1079
Qy 155 AAGTTGAAGTACTTGATGAGAAAGCATGGAACCGGTTACACTCCATCGACATCTCT 214
Db 1080 AAGTTGAAGTACTTGATGAGAAAGCATGGAACCGGTTACACTCCATCGACATCTCT 1139

Qy 215 TGTCTTGAACAGATTTCTCTCAGAGATTCGTCAGGTCGTGGTGTCTCGGAC 274
Db 1140 TGTCTTGAACAGATTTCTCTCAGAGATTCGTCAGGTCGTGGTGTCTCGGAC 1199
Qy 275 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGGAATGCAATTCCTGGTGA 334
Db 1200 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGGAATGCAATTCCTGGTGA 1259
Qy 335 TTGAGCAGTTGATCAACCAAGAGATCGAAGATTCGCGAAGAACCAAGCCATCTAGT 394
Db 1260 TTGAGCAGTTGATCAACCAAGAGATCGAAGATTCGCGAAGAACCAAGCCATCTAGT 1319
Qy 395 TGAAGGATTTGAGCAATCTCTACCAAAATCTATGACAGAGCTTCAGAGTGGAGCCG 454
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Db 1500 TGTAGCTTCAAGCACTATCTTCACTCAGCGTCTTCGAGACCTTAGCCTGTTGGGC 1559
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Qy 935 TCCGTGTTCTGCCAAGATTCGAAGGCTTCATCAGAGCCCACTTATGATGACATCT 994
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Qy 1055 AGATCATGAGCTCTTCAAGTTGATTCAGCGGCGCGAGTTTACCTTCTCTATGAGAA 1114
Db 1980 AGATCATGAGCTCTTCAAGTTGATTCAGCGGCGCGAGTTTACCTTCTCTATGAGAA 2039
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Qy 1175 GAACCTGTCTTCAACCTTGTACAGAGACCTTCAATATGAGTATCAACACGACAC 1234
Db 2100 GAACCTGTCTTCAACCTTGTACAGAGACCTTCAATATGAGTATCAACACGACAC 2159
Qy 1235 TTTTCGTTCTTGAAGGAAAGAGTTGCTATGAAACCTCTTCTTACTTGCATTCGCTG 1294
Db 2160 TTTTCGTTCTTGAAGGAAAGAGTTGCTATGAAACCTCTTCTTACTTGCATTCGCTG 2219

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Db	2280	TGCCACCCAGGCGAAGGATTCCTCCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGAT	2339
Oy	1415	TCAGCAACAGTTCGGTGGCATCATCAGGCTCCGATGTTCTCATGGATTCATGTAAGT	1474
Db	2340	TCAGCAACAGTTCGGTGGCATCATCAGGCTCCGATGTTCTCATGGATTCATGTAAGT	2399
Oy	1475	CTGAGTTCAACAAATATCATTCCTTCTCTCAATATCCCAATCCCATTTGACCAAGTCTA	1534
Db	2400	CTGAGTTCAACAAATATCATTCCTTCTCTCAATATCCCAATCCCATTTGACCAAGTCTA	2459
Oy	1535	CTAACCTTGGATCTGGAACTTCGTGCGTGAAGAAGCCAGGCTTCACAGGAGTGAATATTC	1594
Db	2460	CTAACCTTGGATCTGGAACTTCGTGCGTGAAGAAGCCAGGCTTCACAGGAGTGAATATTC	2519
Oy	1595	TTAGAGAATCTTCTCTGGCCAGATTTAGACACCTCAGAGTTAACATCATCTGCACACCTT	1654
Db	2520	TTAGAGAATCTTCTCTGGCCAGATTTAGACACCTCAGAGTTAACATCATCTGCACACCTT	2579
Oy	1655	CTCAAGATATCGTGTCAAGATTGTTACGCATCTACCATTAATTGCAATTTCCACACTT	1714
Db	2580	CTCAAGATATCGTGTCAAGATTGTTACGCATCTACCATTAATTGCAATTTCCACACTT	2639
Oy	1715	CCATGACGGAAGGCGTATCATCATCGGGTAACCTTCGCGAACCATGTGCAAGCGGACAGA	1774
Db	2640	CCATGACGGAAGGCGTATCATCATCGGGTAACCTTCGCGAACCATGTGCAAGCGGACAGA	2699
Oy	1775	ACTTGCATTCGGCGAGCTTCAGAACCGTGGGTTTCATCTCTTTCACCTTCTTAAAG	1834
Db	2700	ACTTGCATTCGGCGAGCTTCAGAACCGTGGGTTTCATCTCTTTCACCTTCTTAAAG	2759
Oy	1835	GATCAAGGTTTTACCCCTTACCGCTACATGTTGTTCAATTTCTGGCAATGAAGTACATTG	1894
Db	2760	GATCAAGGTTTTACCCCTTACCGCTACATGTTGTTCAATTTCTGGCAATGAAGTACATTG	2819
Oy	1895	ACCGTATTGAGTTTGCTGCTGCGGAAGTTACCTTTGAGGCTGAGTACTGAGAAATTCATGC	1954
Db	2820	ACCGTATTGAGTTTGCTGCTGCGGAAGTTACCTTTGAGGCTGAGTACTGAGAAATTCATGC	2879
Oy	1955	T 1955	
Db	2880	T 2880	

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1  RESULT 4
2  US-09-328-473-9
3  , Sequence 9, Application US/09328473
4  , Patent No. 623253
5  , GENERAL INFORMATION:
6  , APPLICANT: Irvin J. Metcalf, Paul S. Dietrich, Ralph Sinibaldi
7  , TITLE OF INVENTION: DNA Construct Containing Bacillus
8  , NUMBER OF SEQUENCES: 11
9  , CORRESPONDENCE ADDRESS:
10 , ADDRESSEE: No. 623253artis Corporation
11 , STREET: 564 Morris Avenue
12 , CITY: Summit
13 , STATE: New Jersey
14 , COUNTRY: USA
15 , ZIP: 07901
16 ,
17 , COMPUTER READABLE FORM:
18 , MEDIUM TYPE: Floppy disk
19 , COMPUTER: IBM PC compatible
20 , OPERATING SYSTEM: PC-DOS/MS-DOS
21 , SOFTWARE: PatentIn Release #1.0, Version #1.25
22 , CURRENT APPLICATION DATA:
23 , APPLICATION NUMBER: US/09/328,473
24 , FILING DATE:
25 , CLASSIFICATION:

```

Query Match	Best Local Similarity	Score	DB 3	Length
Matches 1853: Conservative	99.6%	1848.2	0	7378
	0	0	8	Indels 0; Gaps 0;
<p>Prior Application Data:</p> <p>Application Number: 09/042,426</p> <p>Filing Date: March 13, 1998</p> <p>Attorney/Agent Information:</p> <p>Name: Hoxie, Thomas</p> <p>Registration Number: 32,993</p> <p>Reference/Docket Number: 135/1</p> <p>Telecommunication Information:</p> <p>Telephone: (919) 541-8614</p> <p>Telefax: (919) 541-8689</p> <p>Information for SEQ ID NO: 9:</p> <p>Sequence Characteristics:</p> <p>Length: 7378 base pairs</p> <p>Type: nucleic acid</p> <p>Strandedness: double</p> <p>Topology: linear</p> <p>Molecule Type: DNA (genomic)</p> <p>Hypothetical: NO</p> <p>Anti-Sense: NO</p> <p>Immediate Source:</p> <p>Clone: Complete sequence of pZ01502</p>				
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155	AAGTTGAAGTACTTGTGTGAGAGACGCAATTGAAACCGGTACATCCCATGCAATCTCT	214		
1080	AAGTTGAAGTACTTGTGTGAGAGACGCAATTGAAACCGGTACATCCCATGCAATCTCT	1139		
215	TGTCCTTGACACAGTTTCTGCTGACGCGAGTTCGTCAGAGGCTGGGTCTGTTCCGAG	274		
1140	TGTCCTTGACACAGTTTCTGCTGACGCGAGTTCGTCAGAGGCTGGGTCTGTTCCGAG	1199		
275	TAGTTGACATCATCTGGGGTACTTGGTCCATCTCAATGGAGATGATCTCTGTCMAA	334		
1200	TAGTTGACATCATCTGGGGTACTTGGTCCATCTCAATGGAGATGATCTCTGTCMAA	1258		
335	TTGAGCAGTTCATTAACGAGAGATTCGAAAGTTCGCGAGAACGAGCCATCTCTAGT	394		
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395	TGGAAGATTGAGCAATCTCTACCAAACTCTATGAGAGAGCTTGAGAGATGGGAAGCG	454		
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455	ATCTCTAACCCACAGCTCTCCGCGAGGAATGCGTATTAATTCACGACATGAAACAGC	514		
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515	CCTTGACCAAGCTATCCCATTTGTTGGCAGTCGAAATACCAAGTTCCTCTGTCGCG	574		
1440	CCTTGACCAAGCTATCCCATTTGTTGGCAGTCGAAATACCAAGTTCCTCTGTCGCG	1499		
575	TGTAAGTTCAAGCAGCTAATCTTCACTCAGCGTGTTCGACGTTAGCGTTTGGGC	634		
1500	TGTAAGTTCAAGCAGCTAATCTTCACTCAGCGTGTTCGACGTTAGCGTTTGGGC	1555		
635	AAAGTGGGGATTGATGCTGCAACCAATCAATAGCGTTTAAACGACCTTCTAGCTGA	694		
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695	TTGGAACCTACACGACGCTGTCTGTTGGTAAACACCTGCTGGAGCGTGTCTGGG	754		
1620	TTGGAACCTACACGACGCTGTCTGTTGGTAAACACCTGCTGGAGCGTGTCTGGG	1679		
755	GTCTGATTTCTAGATTGGATTAGTCAACCAAGTTGAGAGAAATTGACCCCTCAG	814		

Db 1680 GTCTGATTTAGAGATTGATTAAGATCAACAGTTCCAGAGAGAAATTCAGCCTCACAG 1739
Qy 815 TTTTGACATGTGTCTCTCTTCCGGAATGATGATCCAGAACTTACCTTCCGTACAG 874
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Qy 875 TGTCCCAACTTACAGAGAAATCTAATCAACCAAGTTCTTGAGAACTTGACGGTAGCT 934
Db 1800 TGTCCCAACTTACAGAGAAATCTAATCAACCAAGTTCTTGAGAACTTGACGGTAGCT 1859
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Db 1860 TCCGTGTTCCGCCAAGGTATCCAAAGGCTCATCAGAGAGCCACACTGATGAGCAACT 1919
Qy 995 TGAACAGATTAATATCTACACAGGATGCTCAGAGAGAGATTAATTAATGCTGAGACAC 1054
Db 1920 TGAACAGATTAATATCTACACAGGATGCTCAGAGAGAGATTAATTAATGCTGAGACAC 1979
Qy 1055 AGATCATGGCCTCTCCAGTTGATTCAGCGGCGCCGAGTTTACCTTCTCTATGGA 1114
Db 1980 AGATCATGGCCTCTCCAGTTGATTCAGCGGCGCCGAGTTTACCTTCTCTATGGA 2039
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Db 2040 CTATGGGAAAAGCGCGCTCCAAACAGTATGTTGCTCACTAGTCAAGGTGAGGTCTACA 2099
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Qy 1235 TTTCCGTTCTTGACGGAAAGAGTTGGCTTATGAACTCTTCTAATCTTCCGTCATCGCTG 1294
Db 2160 TTTCCGTTCTTGACGGAAAGAGTTGGCTTATGAACTCTTCTAATCTTCCGTCATCGCTG 2219
Qy 1295 TTTTACAGAAAGCGGAAACCGTTGATTCCTTGAGAGAAATCCACAGAGAAACAGATG 1354
Db 2220 TTTTACAGAAAGCGGAAACCGTTGATTCCTTGAGAGAAATCCACAGAGAAACAGATG 2279
Qy 1355 TGCCACCCAGGCAAGATTTCTCCACAGAGTTGAGCCAGCTGCTCATGTTCCGTTCCGAT 1414
Db 2280 TGCCACCCAGGCAAGATTTCTCCACAGAGTTGAGCCAGCTGCTCATGTTCCGTTCCGAT 2339
Qy 1415 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGTG 1474
Db 2340 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGTG 2399
Qy 1475 CTGAGTTCAACATATCATTTCTTCTCTCAAAATACCCAAATCCCATTTGACCAAGTCTA 1534
Db 2400 CTGAGTTCAACATATCATTTCTTCTCTCAAAATACCCAAATCCCATTTGACCAAGTCTA 2459
Qy 1535 CTAACTTGGATCTGGAACCTTCTGCTGAAAGAGACAGGCTTCACAGAGGATGATTTTC 1594
Db 2460 CTAACTTGGATCTGGAACCTTCTGCTGAAAGAGACAGGCTTCACAGAGGATGATTTTC 2519
Qy 1595 TTAGAAGAACTTCTCTGCGCAAGATTAGCACTTCAGAGTTAATCATCTGCAACCACTT 1654
Db 2520 TTAGAAGAACTTCTCTGCGCAAGATTAGCACTTCAGAGTTAATCATCTGCAACCACTT 2579
Qy 1655 CTCAAAAGATATGTTGATGAGATTTCTGTTAGCATCTAACAATTTGCAATTTCCACACT 1714
Db 2580 CTCAAAAGATATGTTGATGAGATTTCTGTTAGCATCTAACAATTTGCAATTTCCACACT 2639
Qy 1715 CCATGAGAGAAAGGCTATCATATCAGAGTAATCTTCTCCGCAACATATGTAAGCGGACAGA 1774
Db 2640 CCATGAGAGAAAGGCTATCATATCAGAGTAATCTTCTCCGCAACATATGTAAGCGGACAGA 2699
Qy 1775 ACTTGAATCCGGCAGCTTCAGAACCGTTCGTTTCACTAATCTTCTTCAACCTTCTTACG 1834
Db 2700 ACTTGAATCCGGCAGCTTCAGAACCGTTCGTTTCACTAATCTTCTTCAACCTTCTTACG 2759
Qy 1835 GATCAAGGTTTCAACCTTACGGCTCATGTTGATTCATCTGAGCAATGAAAGTATGATTG 1894
Db 2760 GATCAAGGTTTCAACCTTACGGCTCATGTTGATTCATCTGAGCAATGAAAGTATGATTG 2819

Qy 1895 ACCGTAATGAGTTTGTCCTGCGGAAGTATACCTTGAGGCTGAGTACTGAGAAATTCATGC 1954
Db 2820 ACCGTAATGAGTTTGTCCTGCGGAAGTATACCTTGAGGCTGAGTACTGAGAAATTCATGC 2879
Qy 1955 T 1955
Db 2880 T 2880

RESULT 5
US-09-330-737-9
; Sequence 9, Application US/09330737
; Patent No. 6232534
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6232534artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330.737
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: Complete sequence of pZ01502
; US-09-330-737-9

Query Match 66.3%; Score 1848.2; DB 3; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 95 CCATGAGCAACCAACCAACATCAAGATGATTCATTAACATGCTTGAATACCCAG 154
Db 1020 CCATGAGCAACCAACCAACATCAAGATGATTCATTAACATGCTTGAATACCCAG 1079
Qy 155 AAGTTGAAGTACTTGTTGAGAGAGCATTTGAACCGTTTACATCTCCATTCGATCTCT 214
Db 1080 AAGTTGAAGTACTTGTTGAGAGAGCATTTGAACCGTTTACATCTCCATTCGATCTCT 1139
Qy 215 TGTCTTGACACAGTTTCTGCTCAGCGAGTTCTGTCACAGTCTGCTGCTGCTTCTCGAG 274
Db 1140 TGTCTTGACACAGTTTCTGCTCAGCGAGTTCTGTCACAGTCTGCTGCTGCTTCTCGAG 1199

REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7378 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Complete sequence of pZO1502
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-329-169-9

Query Match 66.3%; Score 1848.2; DB 4; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 95 CCATGACACAAACCCAAACATCAAGATGCATTCATACACTGCTTGAGTAAACCGAG 154
DB 1020 CCATGACACAAACCCAAACATCAAGATGCATTCATACACTGCTTGAGTAAACCGAG 1079
QY 155 AAGTTGAAGTACTGGTGGAGAAAGCATTTGAAACCGGTTACATCCCATCGACATCTCT 214
DB 1080 AAGTTGAAGTACTGGTGGAGAAAGCATTTGAAACCGGTTACATCCCATCGACATCTCT 1139
QY 215 TGTCCCTGACACAGTTTCTGCTCAGCAGAGTTGTCGCCAGTGCTGGTTCGTTCTCGGAC 274
DB 1140 TGTCCCTGACACAGTTTCTGCTCAGCAGAGTTGTCGCCAGTGCTGGTTCGTTCTCGGAC 1199
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QY 395 TGGAGAGTTGAGCAATCTCAACAAATCTATGACAGAGCTTTCAGAGTGGGAAAGCG 454
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DB 1560 AAAAGTGGGAGTTGATGCTGCAACCATCAATAGCCGTTTACAGCACTTACTAGCTGA 1619
QY 695 TTGAAAACCTACACGCAACGCTGTTGTTGGTGAACAACCTGGTTGAGCGTGTGCGG 754
DB 1620 TTGAAAACCTACACGCAACGCTGTTGTTGGTGAACAACCTGGTTGAGCGTGTGCGG 1679
QY 755 GTCTGATTTAGAGATTGATTGATTAGTACCAACCAAGTTTCAGAGAGAGATTGACCTCAG 814
DB 1680 GTCTGATTTAGAGATTGATTGATTAGTACCAACCAAGTTTCAGAGAGAGATTGACCTCAG 1739
QY 815 TTTTGGACATTTGTGTCTCTCTTCCGGAATATGATCTCCGAACCTTACCTTACCGTACG 874

DB 1740 TTTTGGACATTTGTGTCTCTCTTCCGGAATATGATCTCCGAACCTTACCTTACCGTACG 1799
QY 875 TGTCCCACTTACAGAGAAATCTATACCAACGAGTTCTTGAGAACTTGACGCGTACGT 934
DB 1800 TGTCCCACTTACAGAGAAATCTATACCAACGAGTTCTTGAGAACTTGACGCGTACGT 1859
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DB 1860 TCCGTGTTCTGCCCAAGTATGCAAGGCTTCATCAGAGCCCACTTGATGACATCT 1919
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DB 1980 AGATCATGGCCTTCCAGTTGATTTACAGCGGCGCCAGTTTACCTTCTCTCTATGAA 2039
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QY 1175 GAACCTTGTCTTCCACCTTGATGACAGAGCCCTTCAATGCGTATCAACACAGCAAC 1234
DB 2100 GAACCTTGTCTTCCACCTTGATGACAGAGCCCTTCAATGCGTATCAACACAGCAAC 2159
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DB 2220 TTTACAGAAAGAGCGGAACCGTTGATTTCTTGAAGAAATCCACACAGAAACAATG 2279
QY 1355 TGCCACACGAGCAAGATTTCTCCACAGTTTGACCAAGTTCATGTTCCGTTCCGAT 1414
DB 2280 TGCCACACGAGCAAGATTTCTCCACAGTTTGACCAAGTTCATGTTCCGTTCCGAT 2339
QY 1415 TCAGCAACAGTTCGCTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATGATG 1474
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DB 2580 CTCAAAGATATGCTGTCAGAGTTGTTAGCATCTACCACTTACTTGAATTTCCACACT 2639
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DB 2640 CCATGACGGAAGGCTATCAATCAGGCTTACTCTCCGCAACCATGTCAGAGCGGACGA 2699
QY 1775 ACTTGCAATCCGCGAGCTTTCAGAAACCGTCCGTTTCACTACTCTTCAACTTCTTAA 1834
DB 2700 ACTTGCAATCCGCGAGCTTTCAGAAACCGTCCGTTTCACTACTCTTCAACTTCTTAA 2759
QY 1835 GATCAAGGTTTTCACCTTACGCTCATGCTGTTCAATTTGCGCAATGAATGATCATTTG 1894
DB 2760 GATCAAGGTTTTCACCTTACGCTCATGCTGTTCAATTTGCGCAATGAATGATCATTTG 2819
QY 1895 ACCGATATGAGTTGTGCTGCGGACCAAGTTACCTTCAAGGCTGAGTACTGAAATTCATGC 1954
DB 2820 ACCGATATGAGTTGTGCTGCGGACCAAGTTACCTTCAAGGCTGAGTACTGAGATCATGAGA 2879

QY 1955 T 1955
Db 2880 T 2880

RESULT 7

US-09-330-714A-9
; Sequence 9, Application US/09330714A
; Patent No. 6342660

GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Simbaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
Thuringiensis Gene

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESS: No. 6342660artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,714A

FILING DATE: 11-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/042,426

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993

REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 7378 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: Complete sequence of pZ01502

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-330-714A-9

Query Match 66.3%; Score 1848.2; DB 4; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 95 CCATGGACAACAACCAACATCAACGAATGATTCATCAACAGCTTGAGTAACCAAG 154
Db 1020 CCATGGACAACAACCAACATCAACGAATGATTCATCAACAGCTTGAGTAACCAAG 1079
QY 155 AAGTTGAAGTACTGTTGGAGAGACGATTGAACCGGTTACACTCCATCGACATCTCT 214
Db 1080 AAGTTGAAGTACTGTTGGAGAGACGATTGAACCGGTTACACTCCATCGACATCTCT 1139
QY 215 TGTCTTGAACAAGTTTCTGCTCAGGAGTTCTGTCAGAGTCTGCTGCTTCTTCGAC 274
Db 1140 TGTCTTGAACAAGTTTCTGCTCAGGAGTTCTGTCAGAGTCTGCTGCTTCTTCGAC 1199
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|||||

Db 1200 TAGTTGACATCATCTGGGATCTTGTGTCATCTCAATGGAGTGCATCTGAGTGA 1259
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Db 1320 TGAAGAGATTGAGCAATCTCTACCAATCTATGAGAGAGCTTGAAGAGTGGAAACCG 1379
QY 455 ATCTACTAACCCAGCTCTCCGGAGAAATGCGATTCAATTCAAGACATGAACAGCG 514
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QY 635 AAAGTGGGAGTTGATGCTGCAACCAATCAATAGCCGTTACAGACCTTACTAGCTGA 694
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Db 1620 TTGGAACCTACACCGACCGCTGTTGTTGTTGAACCACTGAGTGGAGCTGTGG 1679
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Db 2040 CTATGGAAGAACCGGCTTCCACAACAGCTATCTGTTCTCACTAGTATGAGTGTCTCA 2099
QY 1175 GAACCTGTCTTCCACTTGTATCAGAGAACCTTCAATATGAGTATCAACCAACAGCAAC 1234
Db 2100 GAACCTGTCTTCCACTTGTATCAGAGAACCTTCAATATGAGTATCAACCAACAGCAAC 2159
QY 1235 TTTCCGTTCTTGAAGGAAAGAGTTGCTATGAACTCTTCTTACTTGCATTCGCTG 1294
Db 2160 TTTCCGTTCTTGAAGGAAAGAGTTGCTATGAACTCTTCTTACTTGCATTCGCTG 2219
QY 1295 TTTTACAGAAAGAGGAAACGTTGATTCCTTGAAGAAATCCACCAAGAAACAAGT 1354
Db 2220 TTTTACAGAAAGAGGAAACGTTGATTCCTTGAAGAAATCCACCAAGAAACAAGT 2279
QY 1355 TGCCACCAAGCAAGATTTCTTCCACAGTTGAGCAGTGTCCATGTTCCGTTCCGAT 1414
Db 2280 TGCCACCAAGCAAGATTTCTTCCACAGTTGAGCAGTGTCCATGTTCCGTTCCGAT 2339

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 QY 1535 CTAACCTTGATCTGGAACCTCTGTCGTAAGAGACAGAGCTTCAAGAGAGTATATTC 1594
 Db 2460 CTAACCTTGATCTGGAACCTCTGTCGTAAGAGACAGAGCTTCAAGAGAGTATATTC 2519
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 Db 2580 CTCAGAAATATCTGTCAGATTTGCTTACGATCTTACCACTTACCTTGAATTTCCACACTT 2639
 QY 1715 CCATGACGAGAGGCTTATCATATCAGGATTAACCTTCTCGCAACCATGTCAGCGGACGCA 1774
 Db 2640 CCATGACGAGAGGCTTATCATATCAGGATTAACCTTCTCGCAACCATGTCAGCGGACGCA 2699
 QY 1775 ACTTGCAATCCGCGAGCTTCAAGAACCGTCCGTTTCACTACTCTTCAACTTCTCTAAAG 1834
 Db 2700 ACTTGCAATCCGCGAGCTTCAAGAACCGTCCGTTTCACTACTCTTCAACTTCTCTAAAG 2759
 QY 1835 GATCAAGGTTTTCACCTTACCGCTCATATGTTTCAATTTGCGCAATGAAGTATCATTTG 1894
 Db 2760 GATCAAGGTTTTCACCTTACCGCTCATATGTTTCAATTTGCGCAATGAAGTATCATTTG 2819
 QY 1895 ACCGATTTGATTTTGTGCTGCGGAGGTTACCTTCAAGAGCTGAGTACTGAGATTCATGC 1954
 Db 2820 ACCGATTTGATTTTGTGCTGCGGAGGTTACCTTCAAGAGCTGAGTACTGAGATTCATGSA 2879
 QY 1955 T 1955
 Db 2880 T 2880

RESULT 8
 US-09-328-826-9
 ; Sequence 9, Application US/09328826
 ; Patent No. 6399860
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
 ; TITLE OF INVENTION: DNA Construct Containing Bacillus
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6399860artis Corporation
 ; STREET: 564 Morris Avenue
 ; CITY: Summit
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07901
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/328,826
 ; FILING DATE: 09-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/042,426
 ; FILING DATE: March 13, 1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoxie, Thomas
 ; REGISTRATION NUMBER: 32,993
 ; REFERENCE/DOCKET NUMBER: 135/1

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 541-8614
 ; TELEFAX: (919) 541-8689
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7378 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; IMMEDIATE SOURCE:
 ; CLONE: Complete sequence of p201502
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-09-328-826-9

Query Match 56.3%; Score 1848.2; DB 4; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 95 CCATGACAAACCAACCAACATCAACGAATGCAATTCATACAACTGCTTGAATACCCAG 154
 Db 1020 CCATGACAAACCAACCAACATCAACGAATGCAATTCATACAACTGCTTGAATACCCAG 1079
 QY 155 AAGTTGAAGTACTTGTGAGAGACGCAATTGAAACCGGTTACACTCCATGACATCTCT 214
 Db 1080 AAGTTGAAGTACTTGTGAGAGACGCAATTGAAACCGGTTACACTCCATGACATCTCT 1139
 QY 215 TGTCTTGAACACATTTCTGCTCAGCGAGTTCCGAGGTCGAGGTCGTTCTCGGAC 274
 Db 1140 TGTCTTGAACACATTTCTGCTCAGCGAGTTCCGAGGTCGAGGTCGTTCTCGGAC 1199
 QY 275 TAGTTGACATCATCTGGGGTATCTTGTGTCATCTCAATGGGATGCAATCTCTGTGCAAA 334
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 QY 335 TTGAGCAGTTGATCAACCAAGAGATCGAAGAGTTCCGAGGACCAAGCCATCTCTAGT 394
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 Db 1380 ATCTTAACCAACCAAGCTCTCCGCGAGGAAATGCGTATTCATTTCAACGACATGAACAGCG 1439
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 QY 575 TGTAGCTTCAAGCAGCTAATCTTCAACCTCAGCGTCTCGAGAGCTTGAAGGTTTGGGC 634
 Db 1500 TGTAGCTTCAAGCAGCTAATCTTCAACCTCAGCGTCTCGAGAGCTTGAAGGTTTGGGC 1559
 QY 635 AAAGTGCGGATTCGATGCTGCAACCAATCAATAGCCGTTTACAGACGACTTCTAGCTGA 694
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 Db 1620 TTGGAATCAACGAGACGACGCTGTTGCTTGTATACACACTGCTTGAAGGTCGTCTGG 1679
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 Db 1680 GTCCGATTTAGAGATTGATTGATTAACAACAGTTTCAAGAGAGAAATTGACCCCTCAGAG 1739
 QY 815 TTTTGACATTTGTCTCTCTTCCGAACTATGACTCCAGAACTTACCTTATCCGTATAG 874
 Db 1740 TTTTGACATTTGTCTCTCTTCCGAACTATGACTCCAGAACTTACCTTATCCGTATAG 1799

QY 875 TGTCCTCACTTACAGAGAAATCTATACCAACCGATTCTTGAGAACTTGCAGCGTAGCT 934
 DB 1800 TGTCCTCACTTACAGAGAAATCTATACCAACCGATTCTTGAGAACTTGCAGCGTAGCT 1859
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 DB 1860 TCCGTGCTTCCGCCAAGGTATCCGAAGGCTCATCAGAGAGCCCACTTGATGACATCT 1919
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 DB 1920 TGAACAGATACATCTATACACCGATGCTCAGAGAGAGATATTACTGTCTGAGACAC 1979
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 DB 2040 CTATGCGGAAAGCGCGCTCCACAACAAGTATCGTTGCTCACTAGGTAGGGTGTCTACA 2099
 QY 1175 GAACCTGTCTTCCACTTGTATCAGAAAGACCTTCAATATGCGTATCAACAACAGCAAC 1234
 DB 2100 GAACCTGTCTTCCACTTGTATCAGAAAGACCTTCAATATGCGTATCAACAACAGCAAC 2159
 QY 1235 TTTTCGTTCTTGACGGAACAGAGTTGCGCTATGAACTCTTCTTACTTCCCATCCGCTG 1294
 DB 2160 TTTTCGTTCTTGACGGAACAGAGTTGCGCTATGAACTCTTCTTACTTCCCATCCGCTG 2219
 QY 1295 TTTTACGAAAGAGCGGAAACCGTGTATCTTGTGAGAGAAATCCCAACAGAAACAGATG 1354
 DB 2220 TTTTACGAAAGAGCGGAAACCGTGTATCTTGTGAGAGAAATCCCAACAGAAACAGATG 2279
 QY 1355 TGCCACCCAGGAGGATTTCTCCACAGATTGAGGCAAGTGTCCATGTTCCGTTCCGAT 1414
 DB 2280 TGCCACCCAGGAGGATTTCTCCACAGATTGAGGCAAGTGTCCATGTTCCGTTCCGAT 2339
 QY 1415 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGTG 1474
 DB 2340 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGTG 2399
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 DB 2400 CTGAGTTCAACAATCATCTCTCTCTCAATATCAACCAATCCCATTTGACCAAGTCTA 2459
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 DB 2460 CTAACTTGGATCTGGAACCTTCTGCTGTAAGAAAGACAGAGCTTCAAGAGGTGATATTC 2519
 QY 1595 TTAGAAGAACTTCTCTGCGCAGATTAGACACCTCAGAGTTAACTCATCTGACACACTTT 1654
 DB 2520 TTAGAAGAACTTCTCTGCGCAGATTAGACACCTCAGAGTTAACTCATCTGACACACTTT 2579
 QY 1655 CTGAAGAAATGCTGTCAGAGATTGCTGTAGAGCATCAACCAACTTGCATATTCACACTT 1714
 DB 2580 CTGAAGAAATGCTGTCAGAGATTGCTGTAGAGCATCAACCAACTTGCATATTCACACTT 2639
 QY 1715 CCATGAGAGGAGGCTCATCAATCAGAGTAACCTTCTCGCAACCATGTCAAGCGGACAGA 1774
 DB 2640 CCATGAGAGGAGGCTCATCAATCAGAGTAACCTTCTCGCAACCATGTCAAGCGGACAGA 2699
 QY 1775 ACTTGCAATCCGGCAGCTTCAAGAACCGTGGTTTCACTACTCTTTCAACCTTCTCAACG 1834
 DB 2700 ACTTGCAATCCGGCAGCTTCAAGAACCGTGGTTTCACTACTCTTTCAACCTTCTCAACG 2759
 QY 1835 GATCAAGGCTTTTACCCCTTAGCGCTCATGTGTTCAATCTTGGAACAATGAGTGCATTTG 1894
 DB 2760 GATCAAGGCTTTTACCCCTTAGCGCTCATGTGTTCAATCTTGGAACAATGAGTGCATTTG 2819
 QY 1895 ACCGTAATGAGTTGTGCTGCGAGATTACCTTCAGAGCTGAGTACTGAGATTCATGTC 1954
 DB 2820 ACCGTAATGAGTTGTGCTGCGAGATTACCTTCAGAGCTGAGTACTGAGATTCATGTC 2879
 QY 1955 T 1955

DB 2880 T 2880
 RESULT 9
 US-09-289-170-9
 ; Sequence 9, Application US/09289170
 ; Patent No. 6573438
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
 ; TITLE OF INVENTION: DNA Construct Containing Bacillus
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6573438artis Corporation
 ; STREET: 564 Morris Avenue
 ; CITY: Summit
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07901
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/289,170
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/042,426
 ; FILING DATE: Match 13, 1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoxie, Thomas
 ; REGISTRATION NUMBER: 32,993
 ; REFERENCE/DOCKET NUMBER: 135/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 541-8614
 ; TELEFAX: (919) 541-8689
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7378 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; IMMEDIATE SOURCE:
 ; CLONE: Complete sequence of pZO1502
 ; US-09-289-170-9
 Query Match 66.3%; Score 1848.2; DB 4; Length 7378;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 95 CCATGAGCAACACCCAAACATCAACGATTCATCTACACTGCTTGATGAAACCCAG 154
 DB 1020 CCATGAGCAACACCCAAACATCAACGATTCATCTACACTGCTTGATGAAACCCAG 1079
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Qy 635 AAAGTGGGAGTTGATGCTGCAACCATCAATAGCGCTTACAGACGCTTACTAGGCTGA 694
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Db 1680 GTCTGATTTCTAGAGATTGATAGATCAACAGCTTACAGAGAGAAATGACCTCAACG 1739
Qy 815 TTTTGGACATTTGTCTCTCTTCCGAACTATGACTCCAGAACTTACTCTGTTAGAC 874
Db 1740 TTTTGGACATTTGTCTCTCTTCCGAACTATGACTCCAGAACTTACTCTGTTAGAC 1799
Qy 875 TGTCCCAACTACAGAGAAATCTATTAATCCAGTCTTGAGAACTTGACGGTATGCT 934
Db 1800 TGTCCCAACTACAGAGAAATCTATTAATCCAGTCTTGAGAACTTGACGGTATGCT 1859
Qy 935 TCCGTGTTCTGCCCAAGGTATCGAAGGCTCCATCAGAGGCCCACTTGAATGACATCT 994
Db 1860 TCCGTGTTCTGCCCAAGGTATCGAAGGCTCCATCAGAGGCCCACTTGAATGACATCT 1919
Qy 995 TGAACAGATTAATCTATCTTCAACCGATGCTCAACAGAGAGAGTATTACTGCTGACAC 1054
Db 1920 TGAACAGATTAATCTATCTTCAACCGATGCTCAACAGAGAGAGTATTACTGCTGACAC 1979
Qy 1055 AGATCATGCGCTTCCCACTTGTGATTCAGCGGCGCGGAGTTTAACTTCTCTATGGA 1114
Db 1980 AGATCATGCGCTTCCCACTTGTGATTCAGCGGCGCGGAGTTTAACTTCTCTATGGA 2039
Qy 1115 CTATGGGAAAGCGCGCTCCACAACACGATTCGTTGCTCAATAGAGTCAAGGCTGCTACA 1174
Db 2040 CTATGGGAAAGCGCGCTCCACAACACGATTCGTTGCTCAATAGAGTCAAGGCTGCTACA 2099
Qy 1175 GAACCTTGTCTTCACTTGTATCAGAGAACCTTCAATATGCGTATCAACACGACAC 1234
Db 2100 GAACCTTGTCTTCACTTGTATCAGAGAACCTTCAATATGCGTATCAACACGACAC 2159
Qy 1235 TTTCCGTTCTTGAAGGAGACAGGTTGCGCTATGSAACCTTCTTCAATTTGCGATCGGCTG 1294
Db 2160 TTTCCGTTCTTGAAGGAGACAGGTTGCGCTATGSAACCTTCTTCAATTTGCGATCGGCTG 2219
Qy 1295 TTTACAGAAAGGCGGAAACCGTTGATTCCTTGAAGAAATCCACACAGAACCAATG 1354
Db 2220 TTTACAGAAAGGCGGAAACCGTTGATTCCTTGAAGAAATCCACACAGAACCAATG 2279
Qy 1355 TGCCACCCAGGAGAGATTTCTCCACAGGTTGAGCCAGTGTCTATGTTCCGTTCCGAT 1414
Db 2280 TGCCACCCAGGAGAGATTTCTCCACAGGTTGAGCCAGTGTCTATGTTCCGTTCCGAT 2339
Qy 1415 TCAGCAACAGTTCCGTTGAGCATCATCAGAGCTCCTATGTTCTCATGAGATTCACTGATG 1474
Db 2340 TCAGCAACAGTTCCGTTGAGCATCATCAGAGCTCCTATGTTCTCATGAGATTCACTGATG 2399

Qy 1475 CTGAGTTCAACAATATCATTTCTTCTCTGTAATTCACCCAAATCCCATTTGACCAAGCTCTA 1534
Db 2400 CTGAGTTCAACAATATCATTTCTTCTCTGTAATTCACCCAAATCCCATTTGACCAAGCTCTA 2459
Qy 1535 CTAACTTGGATCTGGAACCTTCTGCTGTAAGGACCAAGGCTTCACAGAGGATATTTG 1594
Db 2460 CTAACTTGGATCTGGAACCTTCTGCTGTAAGGACCAAGGCTTCACAGAGGATATTTG 2519
Qy 1595 TTGAGAGAACTTCTCTGCGCGAGATTAGCAACCTCAGAGTTTAAATCATCATGACACCTTT 1654
Db 2520 TTGAGAGAACTTCTCTGCGCGAGATTAGCAACCTCAGAGTTTAAATCATCATGACACCTTT 2579
Qy 1655 CTCAAGATATGCTGTGAGGATTCGTGATGATGATGATGATGATGATGATGATGATGATG 1714
Db 2580 CTCAAGATATGCTGTGAGGATTCGTGATGATGATGATGATGATGATGATGATGATGATG 2639
Qy 1715 CCATCGACGGAAGGCTTATCAATCAAGGTTAACTTCTCCGAAACCATGTCAGAGGCGAGCA 1774
Db 2640 CCATCGACGGAAGGCTTATCAATCAAGGTTAACTTCTCCGAAACCATGTCAGAGGCGAGCA 2699
Qy 1775 ACTTGCAATCCGCGAGCTTCAGAACCGTCCGTTTCACTACTCTTCAACTTCTCTAACG 1834
Db 2700 ACTTGCAATCCGCGAGCTTCAGAACCGTCCGTTTCACTACTCTTCAACTTCTCTAACG 2759
Qy 1835 GATCAAGCGTTTTCACCTTAGCGGCTCATGTTCAATTTCTGCAATGAAAGTTACATTG 1894
Db 2760 GATCAAGCGTTTTCACCTTAGCGGCTCATGTTCAATTTCTGCAATGAAAGTTACATTG 2819
Qy 1895 ACCGATTTGATTTGTCCTGCGGAAGTTACCTTCGAGGCTGAGTACTGAGAAATTCATGC 1954
Db 2820 ACCGATTTGATTTGTCCTGCGGAAGTTACCTTCGAGGCTGAGTACTGAGAAATTCATGC 2879
Qy 1955 T 1955
Db 2880 T 2880

RESULT 10
US-09-042-426-3
; Sequence 3, Application US/09042426
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6114608artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1851 base pairs
; TYPE: nucleic acid

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: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: c171ab toxic gene region
US-09-042-426-3

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Query Match	66.2%;	Score 1845.4;	DB 3;	Length 1851;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1846;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

OY	96	CATGACAACAACCCAAACATCAAGAAATGCAATTCATCACTCAACTGTTAGTAAACCGA	155
Db	1	CATGACAACAACCCAAACATCAAGAAATGCAATTCATCACTGTTAGTAAACCGA	60
OY	156	AGTTGAAGTACTTGGTGGAGAAACGATTTGAAACCGGTTACATCCCATGACATCTCCTT	215
Db	61	AGTTGAAGTACTTGGTGGAGAAACGATTTGAAACCGGTTACATCCCATGACATCTCCTT	120
OY	216	GTCCCTTGACACAGTTTCTGCTCAGCGAGTTCGTCGAGGTGCTGGGTTGCTTCGGAAT	275
Db	121	GTCCCTTGACACAGTTTCTGCTCAGCGAGTTCGTCGAGGTGCTGGGTTGCTTCGGAAT	180
OY	276	AGTTGACATCATCTGGGGATCTTTGGTCCATCTCAATGGAGTGCATTCCTGGTGCAAAT	335
Db	181	AGTTGACATCATCTGGGGATCTTTGGTCCATCTCAATGGAGTGCATTCCTGGTGCAAAT	240
OY	336	TGAGCAGATTGATCAACCAAGAGATGGAAGATTTCCGACAGAAACGAGGCCATCTCTAGGTT	395
Db	241	TGAGCAGATTGATCAACCAAGAGATGGAAGATTTCCGACAGAAACGAGGCCATCTCTAGGTT	300
OY	396	GGAAGATTTGAGCAGATCTCTCAACCAATCTATCAGAGAGCTTCAGAGATGGGAAGCCGA	455
Db	301	GGAAGATTTGAGCAGATCTCTCAACCAATCTATCAGAGAGCTTCAGAGATGGGAAGCCGA	360
OY	456	TCTTAATAACCCAGCTCTTCGCGAGAAATGCGATTTCAATTCACGACATGAAACAGCC	515
Db	361	TCTTAATAACCCAGCTCTTCGCGAGAAATGCGATTTCAATTCACGACATGAAACAGCC	420
OY	516	CTTGACACAGCTATCCCATGTTGTCGCACTCCAGAACTCAACAGTCCCTCTGTCGGT	575
Db	421	CTTGACACAGCTATCCCATGTTGTCGCACTCCAGAACTCAACAGTCCCTCTGTCGGT	480
OY	576	GTACGTTCAAGCAGCTAATCTTCAACCTCAGCGTCTTGAGACGTTAGCGGTGTTGGGA	635
Db	481	GTACGTTCAAGCAGCTAATCTTCAACCTCAGCGTCTTGAGACGTTAGCGGTGTTGGGA	540
OY	636	AAGGTGGGATTCGATGCTGCAACCATCAATAGCCCTTCAACAGACTTACTAGGCTGAT	695
Db	541	AAGGTGGGATTCGATGCTGCAACCATCAATAGCCCTTCAACAGACTTACTAGGCTGAT	600
OY	696	TGGAACCTACACCGACCAACGCTGTTGCTGTTGATCAACACTGGCTTGAGCGTGTCTGGG	755
Db	601	TGGAACCTACACCGACCAACGCTGTTGCTGTTGATCAACACTGGCTTGAGCGTGTCTGGG	660
OY	756	TCCTGATTTAGAGATTGATTAAGATACAAACGATTCAGAGAGAAATGACCTTCAAGT	815
Db	661	TCCTGATTTAGAGATTGATTAAGATACAAACGATTCAGAGAGAAATGACCTTCAAGT	720
OY	816	TTTGGACATTGATGCTCTCTTCCGGAATATGCTCAGAACTTACCTTCCGTACAGT	875
Db	721	TTTGGACATTGATGCTCTCTTCCGGAATATGCTCAGAACTTACCTTCCGTACAGT	780
OY	876	GTCCCAACTTACCAAGAAATCTATACTAACCCAGTTCTTGAGACCTTCGACGGTAGCTT	935
Db	781	GTCCCAACTTACCAAGAAATCTATACTAACCCAGTTCTTGAGACCTTCGACGGTAGCTT	840
OY	936	CGGTGGTTCCGCCAAGATATGAAGGCTCATCAGAGGCCACACTGATGACATCTT	995
Db	841	CGGTGGTTCCGCCAAGATATGAAGGCTCATCAGAGGCCACACTGATGACATCTT	900

Qy	996	GAACAGACATACATATATACACCGATGTCTCAGAGAGATATATACGTCTGGACACCA	1055
Db	901	GAACAGCATATACATCTACACCGATGTCTCAGAGAGATATATACGTCTGGACACCA	960
Qy	1056	GATCATGAGCCTCTCCAGATGGATTCAGCGGAGCCCGAGATTACCTTCTCTCTATGAAAC	1115
Db	961	GATCATGAGCCTCTCCAGATGGATTCAGCGGAGCCCGAGATTACCTTCTCTCTATGAAAC	1020
Qy	1116	TATGGGAAAGCGCGCTCCACAACAGATATGTTGTCCTCAACTAGGTAGGGGTCTACAG	1175
Db	1021	TATGGGAAAGCGCGCTCCACAACAGATATGTTGTCCTCAACTAGGTAGGGGTCTACAG	1080
Qy	1176	AACCTTGCTCTTCCACTTGTATACAGAAAGACCCCTTCAATATCGTATCAACAACAGCACT	1235
Db	1081	AACCTTGCTCTTCCACTTGTATACAGAAAGACCCCTTCAATATCGTATCAACAACAGCACT	1140
Qy	1236	TTCCGCTCTTGAAGGAAACAGAGTTCGGCTATAGAAACCTCTTCTTCACTTGGCATCCGCTGT	1295
Db	1141	TTCCGCTCTTGAAGGAAACAGAGTTCGGCTATAGAAACCTCTTCTTCACTTGGCATCCGCTGT	1200
Qy	1296	TTACAGAAAGAGCGGAAACCGTGTGATTCCTTGGAGAAATCCACACAGAAACAACAATGT	1355
Db	1201	TTACAGAAAGAGCGGAAACCGTGTGATTCCTTGGAGAAATCCACACAGAAACAACAATGT	1260
Qy	1356	GCCACCCAGGCAAGGATTTCTCCACAGGTTGAGCCACGCTGCCATGTTCCGTTCCGATT	1415
Db	1261	GCCACCCAGGCAAGGATTTCTCCACAGGTTGAGCCACGCTGCCATGTTCCGTTCCGATT	1320
Qy	1416	CAGCAACAGTTCGGTGGAGCATCAACAGAGTCCATGTTCTCAGAGATTCATCGTAGAGC	1475
Db	1321	CAGCAACAGTTCGGTGGAGCATCAACAGAGTCCATGTTCTCAGAGATTCATCGTAGAGC	1380
Qy	1476	TGAATTCAACAATATTCATTTCTTCTCTCTCAAAATCACCCTAATCCCATTTGACCAAGTCTAC	1535
Db	1381	TGAATTCAACAATATTCATTTCTTCTCTCTCAAAATCACCCTAATCCCATTTGACCAAGTCTAC	1440
Qy	1536	TAACTTGGATCTGGAACCTTGTGTCGTGAAAGAACAGGCTTTCACAGAGGTGATATCT	1595
Db	1441	TAACTTGGATCTGGAACCTTGTGTCGTGAAAGAACAGGCTTTCACAGAGGTGATATCT	1500
Qy	1596	TAGAAAGAACTCTCTGGGCGAGATTAGAACCCCTCAGAGTTAAACATCACTGACACACTTC	1655
Db	1501	TAGAAAGAACTCTCTGGGCGAGATTAGAACCCCTCAGAGTTAAACATCACTGACACACTTC	1560
Qy	1656	TCAAAAGATATCGTGCAGAGATTGTTACGATCTACACTAATTGCAATTTCCACACTC	1715
Db	1561	TCAAAAGATATCGTGCAGAGATTGTTACGATCTACACTAATTGCAATTTCCACACTC	1620
Qy	1716	CATGACGGAAGGCGCTATCATCAAGGGTAACTTCTCCGCAACCATATGTAAGCGGACGAA	1775
Db	1621	CATGACGGAAGGCGCTATCATCAAGGGTAACTTCTCCGCAACCATATGTAAGCGGACGAA	1680
Qy	1776	CTTGCAATCCGGACAGCTTCAGAACCGTGGATTCACTACTCTTTTCAACTTCTCTTACCGG	1835
Db	1681	CTTGCAATCCGGACAGCTTCAGAACCGTGGATTCACTACTCTTTTCAACTTCTCTTACCGG	1740
Qy	1836	ATCAAGCGTTTTCACCCCTTAGCGCTCATGTTTCAAATTCGCGCAATGSAAGTGTACATGGA	1895
Db	1741	ATCAAGCGTTTTCACCCCTTAGCGCTCATGTTTCAAATTCGCGCAATGSAAGTGTACATGGA	1800
Qy	1896	CCGATTTAGTTTGTGCTGCGGAAAGTTACCTTCGAGGCTGAGTACT 1942	
Db	1801	CCGATTTAGTTTGTGCTGCGGAAAGTTACCTTCGAGGCTGAGTACT 1847	
RESULT 11			
US-09-291-238-3			
; Sequence 3, Application US/09291238			
; Patent No. 622104			
GENERAL INFORMATION:			
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi			
TITLE OF INVENTION: DNA Construct Containing Bacillus			
NUMBER OF SEQUENCES: 11			

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; RESULT 11
; US-09-291-238-3
; Sequence 3, Application US/09291238
; Patent No. 6222104
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11

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CORRESPONDENCE ADDRESS:
ADDRESS: No. 622104artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cry1ab toxic gene region
US-09-291-238-3

Query Match 66.2%; Score 1845.4; DB 3; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 96 CATGACAAACCCAAACATCAAGATGATTCATCAACATCTTGAGTAAACCCAGA 155
DB 1 CATGACAAACCCAAACATCAAGATGATTCATCAACATCTTGAGTAAACCCAGA 60
QY 156 AGTTGAAGTACTTGGTGAAGAACGATTTGAAACCGGTTACACTCCCATGACATCTCCTT 215
DB 61 AGTTGAAGTACTTGGTGAAGAACGATTTGAAACCGGTTACACTCCCATGACATCTCCTT 120
QY 216 GTCCCTGACACAGTTCTGCTCAGGAGTGTGTCAGGAGTGTGAGTTCTTGAGTAA 275
DB 121 GTCCCTGACACAGTTCTGCTCAGGAGTGTGTCAGGAGTGTGAGTTCTTGAGTAA 180
QY 276 AGTTGACATCACTGCGGATCTTTGTTCATCTCAATGGAATGATTCCTGGTCAAT 335
DB 181 AGTTGACATCACTGCGGATCTTTGTTCATCTCAATGGAATGATTCCTGGTCAAT 240
QY 336 TGAGCAGTTGATCAACCAAGAGATGGAAGATTTCCGCAAGAACCGGATCTTCAAGTT 395
DB 241 TGAGCAGTTGATCAACCAAGAGATGGAAGATTTCCGCAAGAACCGGATCTTCAAGTT 300
QY 396 GGAAGGATTTGAGCAATCTCTCAACCAATCTATGACAGAGCTTCAGAGAGTGGAGACGA 455
DB 301 GGAAGGATTTGAGCAATCTCTCAACCAATCTATGACAGAGCTTCAGAGAGTGGAGACGA 360
QY 456 TCTTAATAACCAAGCTCTTCCGCGAGAGAAATGCGTATTCATTTCAATCAACGATCAACAGCGC 515
DB 361 TCTTAATAACCAAGCTCTTCCGCGAGAGAAATGCGTATTCATTTCAATCAACGATCAACAGCGC 420
QY 516 CTTGACCAACAGCTATTCCTGTTGTCAGAGTCCAGAACTTCAAGTTCTCTTTCCTTCCGT 575

DB 421 CTTGACCAACAGCTATTCCTATTTGTCGAGATCCAGACTACCAAGTTCTCTTGTCCGT 480
QY 576 GTAGCTTCAAGACGATTAATCTTCACTCAGCGTCTTGAGACGTTAGCGTTTGGGCA 635
DB 481 GTAGCTTCAAGACGATTAATCTTCACTCAGCGTCTTGAGACGTTAGCGTTTGGGCA 540
QY 636 AAGTGGGAGTTGATGCTGCAACCAATCAATAGCCGTTTACAGACGTTACTAGCTGAT 695
DB 541 AAGTGGGAGTTGATGCTGCAACCAATCAATAGCCGTTTACAGACGTTACTAGCTGAT 600
QY 696 TGAAGTCTACACGACCAACGCTGTTGTTGTTGTAACAACCTGGCTTGAAGCGTCTGGGG 755
DB 601 TGAAGTCTACACGACCAACGCTGTTGTTGTTGTAACAACCTGGCTTGAAGCGTCTGGGG 660
QY 756 TCCGATTTCTAGAGATTGATGATTAATCAACCAAGTTGAGAGAAATTTGACCTTACAGT 815
DB 661 TCCGATTTCTAGAGATTGATGATTAATCAACCAAGTTGAGAGAAATTTGACCTTACAGT 720
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DB 721 TTTGAGACATTTGATCTCTTCCGAACTATGATCCAGAACTTACCTTATCCGTACGT 780
QY 876 GTCCCACTTACAGAGAAATCTATTAACCCAGTTCTTGAAGAACTTCCAGCGTACTT 935
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DB 1021 TATGGAAGACCGCCTCCACAAACGATGCTGCTCAACCTAGGTGCTCTACAG 1080
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DB 1081 AACCTTGTCTTCAACCTTTGACAGAGACCTTCAATTCGGTATCAACCAACGAACT 1140
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DB 1201 TTAAGAAAGAGCGGAACCGTTGATTCCTTGAAGGAATCCACACAGAAACCAATGT 1260
QY 1356 GCCACCCAGGCAAGGATTTCCCAACGTTGAGCCAAGTTCATGTTCCGTTCCGAAAT 1415
DB 1261 GCCACCCAGGCAAGGATTTCCCAACGTTGAGCCAAGTTCATGTTCCGTTCCGAAAT 1320
QY 1416 CAGCAACGTTCCGAGACATCAAGAGCTCTATGTTCTCATGAGATTCAATCGTAGAGC 1475
DB 1321 CAGCAACGTTCCGAGACATCAAGAGCTCTATGTTCTCATGAGATTCAATCGTAGAGC 1380
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DB 1381 TGAGTTCAACATATCATTTCTTCTCTCAATCAACCCAAATCCCATTTGACCAAGCTTAC 1440
QY 1536 TAACTTGAATCTGGAATCTTCTGTCGTGAAGACACAGCTTCAACAGAGTGAATATCT 1595
DB 1441 TAACTTGAATCTGGAATCTTCTGTCGTGAAGACACAGCTTCAACAGAGTGAATATCT 1500
QY 1596 TAGAAGAACTTCTCTGCGCAGATTTAGCAACCTCAGAGTTTAAATCATCTGACCACTTTC 1655
DB 1501 TAGAAGAACTTCTCTGCGCAGATTTAGCAACCTCAGAGTTTAAATCATCTGACCACTTTC 1560

QY 1656 TCAAGATATGCTGACAGATTGCTTACGATCTACCACTAATTCGAATTCACACCTC 1715
DB 1561 TCAAGATATGCTGACAGATTGCTTACGATCTACCACTAATTCGAATTCACACCTC 1620
QY 1716 CATGACGGAAGGCTTATCAATCAAGGTAACCTTCTCCGCAACATGTCAGCGGACGCA 1775
DB 1621 CATGACGGAAGGCTTATCAATCAAGGTAACCTTCTCCGCAACATGTCAGCGGACGCA 1680
QY 1776 CTTCGAATCCGGGAGCTTACAGACCGTGGTTCACTACCTCTTCAACTCTTAAACG 1835
DB 1681 CTTCGAATCCGGGAGCTTACAGACCGTGGTTCACTACCTCTTCAACTCTTAAACG 1740
QY 1836 ATCAAGCGTTTTCACCCCTTACGCGTCAATGTTCAATTCGCAATGAGTGTACATTGA 1895
DB 1741 ATCAAGCGTTTTCACCCCTTACGCGTCAATGTTCAATTCGCAATGAGTGTACATTGA 1800
QY 1896 CCGTATGAGTTTGTGCTGCTGCCGAAGTTACCTTGAGGCTGAGTACT 1942
DB 1801 CCGTATGAGTTTGTGCTGCTGCCGAAGTTACCTTGAGGCTGAGTACT 1847

RESULT 12

US-09-330-760-3
Sequence 3, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cry1ab toxic gene region
US-09-330-760-3

Query Match 66.2%; Score 1845.4; DB 3; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 96 CATGACACCAACCCAAACATCAACGAATGATTCCTACATCACTGCTTGAATACCGAGA 155
DB 1 CATGACACCAACCCAAACATCAACGAATGATTCCTACATCACTGCTTGAATACCGAGA 60
QY 156 AGTTGAAGTACTTGTGTGAAGAACGCAATTGAACCGGTTACACTCCCATCGACATCTCCTT 215
DB 61 AGTTGAAGTACTTGTGTGAAGAACGCAATTGAACCGGTTACACTCCCATCGACATCTCCTT 120
QY 216 GTCTTGACACAGTTTGTGCTCAGCGAGTTGTCGCCAGTGTGGTTCGTTCTCGGACT 275
DB 121 GTCTTGACACAGTTTGTGCTCAGCGAGTTGTCGCCAGTGTGGTTCGTTCTCGGACT 180
QY 276 AGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAAATGGAATGATTCCTGTGCAAT 335
DB 181 AGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAAATGGAATGATTCCTGTGCAAT 240
QY 336 TGAGCACTGATATCAACAGAGAGATCGAAGAGTTCCGAGGAACCGACCAATCTCTAGATT 395
DB 241 TGAGCACTGATATCAACAGAGAGATCGAAGAGTTCCGAGGAACCGACCAATCTCTAGATT 300
QY 396 GGAAGATGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGATGGAAGCGGA 455
DB 301 GGAAGATGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGATGGAAGCGGA 360
QY 456 TCTCTAATACCCAGCTCTCCGCGAGGAATGCGTATTCATTCACAGCATGAACAGCGC 515
DB 361 TCTCTAATACCCAGCTCTCCGCGAGGAATGCGTATTCATTCACAGCATGAACAGCGC 420
QY 516 CTTCGACACAGCTATCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTGTGCGT 575
DB 421 CTTCGACACAGCTATCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTGTGCGT 480
QY 576 GTAGCTCAAGCAGCTATCTTCACTCAGCGTCTTCAGACGCTTACCGTGTGGAACA 635
DB 481 GTAGCTCAAGCAGCTATCTTCACTCAGCGTCTTCAGACGCTTACCGTGTGGAACA 540
QY 636 AAGGTGGGATTTGATGCTCTGCAACCATCATATAGCCGTTACAGCACTTACGCTGAT 695
DB 541 AAGGTGGGATTTGATGCTCTGCAACCATCATATAGCCGTTACAGCACTTACGCTGAT 600
QY 696 TGGAACTACACCGACCAACGCTGTTGTTGGTAAACACTGGGCTTGGAGGCTGTGGGG 755
DB 601 TGGAACTACACCGACCAACGCTGTTGTTGGTAAACACTGGGCTTGGAGGCTGTGGGG 660
QY 756 TCTGATTTAGAGATTGATTAGATCAACCAAGTTCAGAGAGAAATGACCTTCACAGT 815
DB 661 TCTGATTTAGAGATTGATTAGATCAACCAAGTTCAGAGAGAAATGACCTTCACAGT 720
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DB 721 TTTGGAATGTTGCTCTCTTCCGAACTATGATCCAGAACTTACCTATCGCTACAGT 780
QY 876 GTCCCACTTACAGAGAAATCTATTAACCAAGTCTTGAAGACTTCAGCGGTAGCTT 935
DB 781 GTCCCACTTACAGAGAAATCTATTAACCAAGTCTTGAAGACTTCAGCGGTAGCTT 840
QY 936 CCGTGTCTTCCCAAGGATTCGAAGGCTTCATCAGAGCCGACACTTGATGACATCTT 995
DB 841 CCGTGTCTTCCCAAGGATTCGAAGGCTTCATCAGAGCCGACACTTGATGACATCTT 900
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Qy	1236	TTCCGCTTCTTGAGCGAAGCAGAGTTTCCGCTATAGAACTTTCTAATTTGCCATCCGCTGT	1295
Db	1141	TTCCGCTTCTTGAGCGAAGCAGAGTTTCCGCTATAGAACTTTCTAATTTGCCATCCGCTGT	1200
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Qy	1416	CAGCAACAGTTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGAGATTTCAATGTAATGC	1475
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Db	1381	TGAGTTCAACATATTCATTTCTTCCCTCTCTCAATATCAACCAATATCCCATTTGACCAAGTCTAC	1440
Qy	1536	TAACTTGTGATCTGGAACCTTCTGTCTGTGAAAGAACAGAGCTTCAACAGAGGTGATATTTCT	1595
Db	1441	TAACTTGTGATCTGGAACCTTCTGTCTGTGAAAGAACAGAGCTTCAACAGAGGTGATATTTCT	1500
Qy	1596	TGAGAAAGATCTCTCTCTGCGCGAATTTAGACACCTCAGAGTTAAATCATCTGTGACGACATTTCT	1655
Db	1501	TGAGAAAGATCTCTCTCTGCGCGAATTTAGACACCTCAGAGTTAAATCATCTGTGACGACATTTCT	1560
Qy	1656	TCAAAAGATATCGTGTCAAGATTTCGTTACGCAATCTACCACTAATCTTGCAATTCACACCTC	1715
Db	1561	TCAAAAGATATCGTGTCAAGATTTCGTTACGCAATCTACCACTAATCTTGCAATTCACACCTC	1620
Qy	1716	CATGAGCGGAAGGCGCTATCAATCAGGGTAACTTTCTCCGCAACCATGTATAACGGGACGAA	1775
Db	1621	CATGAGCGGAAGGCGCTATCAATCAGGGTAACTTTCTCCGCAACCATGTATAACGGGACGAA	1680
Qy	1776	CTTGCAATCCGGGACGCTTCAGAAACGATGCGTTTCACTACTCTCTTTCACACTTCTCTAAACG	1835
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RESULT 13			
DS-09-328-473-3			
: Sequence 3, Application US/09328473			
: Patent No. 6232533			
: GENERAL INFORMATION:			
: APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi			
: TITLE OF INVENTION: DNA Construct Containing Bacillus			
: NUMBER OF SEQUENCES: 11			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: No. 623253artis Corporation			
: STREET: 564 Morris Avenue			
: CITY: Summit			
: STATE: New Jersey			
: COUNTRY: USA			
: ZIP: 07901			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patentin Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			

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Db 1	CATGAGACAAACCCAAACATCAACGAATGCATTCATCAACATCTGTTAGTAACCCAGA	60					
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Db 121	GTCCCTTGACACAGTTTCTGCTCAGCGAATTCGTGCGAGTCTGGGTTGTTCTTGGACT	180					
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Db 181	AGTTGACATCATCTGGGGTATCTTTGGTTCATCTCAATGGGATGATTCCTGGTCCAAAT	240					
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Db 421	CTTGACCAACAGCTATCCCATTTGTTGCGAGTCCAGAACCTACCAAGTTCTCTCTTCCGT	480					
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Db 481	GTAAGTTTAAAGCAGTTAATCTTCAACTCAAGGTGTTTGAACCGTTAAGCGTTTGGGGA	540					
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QY 756 TCCTGATTTGAGAGATTGGATTAGATACACAGGTCAGAGAGAAATTGACCTCTCACAGT 815
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 DB 1081 AACCTTGCTTCCACTTGTACAGAAAGCCCTTGAATGCGGTATGCAACACCGCACT 1140
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 RESULT 14
 US-09-330-737-3
 ; Sequence 3, Application US/09330737
 ; Patent No. 6232534
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
 ; TITLE OF INVENTION: DNA Construct Containing Bacillus
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6232534artis Corporation
 ; STREET: 564 Morris Avenue
 ; CITY: Summit
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07901
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/330.737
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/042.426
 ; FILING DATE: March 13, 1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoxie, Thomas
 ; REGISTRATION NUMBER: 32,993
 ; REFERENCE/DOCKET NUMBER: 135/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 541-8614
 ; TELEFAX: (919) 541-8689
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1851 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEetical: NO
 ; ANTI-SENSE: NO
 ; IMMEDIATE SOURCE:
 ; CLONE: cry1Ab toxic gene region
 US-09-330-737-3
 Query Match 66.2%; Score 1845.4; DB 3; Length 1851;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 96 CATGACAAACCAACCAATCAACGAATGATTCATACAACTGTAAGTAAATCCGCA 155
 DB 1 CATGACAAACCAACCAATCAACGAATGATTCATACAACTGTAAGTAAATCCGCA 60
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Db 181 AGTGGACATCATCTGGGGTATCTTGTGCTCAATGGGATGGATTCCTCGTGGCAAT 240
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Db 1081 AACCTTGTCTTCCACTTGTATGAGAAACCTTCAATATCGTATCAACACGAGCACT 1140
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Db 1741 ATCAAGCTTTTCAACCTTACGCTGATGTTTCAATTTCTGGAATGAAGTATCATTTGA 1800
Qy 1896 CCGTATTGATTGTGCTGCGGAGGTTTACCTTGAAGGCTGAGTACT 1942
Db 1801 CCGTATTGATTGTGCTGCGGAGGTTTACCTTGAAGGCTGAGTACT 1847

RESULT 15
US-09-329-169-3
Sequence 3, Application US/09329169
Patent No. 6329575
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6329575artlis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329.169
FILING DATE: 09-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042.426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689


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: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1851 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: cry1Ab toxic gene region
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-329-169-3

Query Match      66.2%; Score 1845.4; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 96 CATGACAAACCCAAACATCAAGAAATGCAATTCATACAACTGCTTGAAGTAACCCAGA 155
DB 1 CATGACAAACCCAAACATCAAGAAATGCAATTCATACAACTGCTTGAAGTAACCCAGA 60
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Search completed: October 21, 2003, 09:46:40
Job time : 194 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 04:39:52 ; Search time 1822 Seconds

(without alignments)
4103.656 Million cell updates/sec

Title: US-09-980-650-6

Perfect score: 2788
Sequence: 1 aataagatcttactgttc.....tactagagatcatatcag 2788

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1843.4	66.1	1845	11	US-09-988-462-5	Sequence 5, Appli
3	1843.4	66.1	3531	12	US-10-102-469-23	Sequence 23, Appli
4	1411.8	50.6	1920	12	US-10-102-469-3	Sequence 3, Appli
5	1411.8	50.6	3534	12	US-10-102-469-9	Sequence 9, Appli
6	1411.8	50.6	3534	12	US-10-102-469-11	Sequence 11, Appli
7	1411.8	50.6	3534	12	US-10-102-469-13	Sequence 13, Appli
8	1328.8	47.7	1767	12	US-10-102-469-5	Sequence 5, Appli
9	1220.4	43.8	4360	9	US-09-756-643-1	Sequence 1, Appli
10	1220	43.8	3468	11	US-09-988-462-1	Sequence 1, Appli
11	1197.6	43.0	3531	14	US-10-035-060-7	Sequence 7, Appli
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14	1180.8	42.4	1743	12	US-10-102-469-1	Sequence 1, Appli
15	1153.8	41.4	1947	11	US-09-988-462-3	Sequence 3, Appli
16	1152.2	41.3	3468	11	US-09-988-462-4	Sequence 4, Appli

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19	1152.2	41.3	3546	11	US-09-988-462-12	Sequence 12, Appli
20	1152.2	41.3	3546	11	US-09-988-462-14	Sequence 14, Appli
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ALIGNMENTS

RESULT 1
US-10-102-469-7
Sequence 7, Application US/10102469
Publication No. US20030192078A1
GENERAL INFORMATION:
APPLICANT: Fischhoff, David A.
TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
FILE REFERENCE: 38-21 (13553) B
CURRENT APPLICATION NUMBER: US/10/102,469
PRIOR APPLICATION NUMBER: 2002-09-05
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: 07/959,506
PRIOR FILING DATE: 1992-10-09
PRIOR APPLICATION NUMBER: 07/476,661
PRIOR FILING DATE: 1990-02-12
PRIOR APPLICATION NUMBER: 07/315,355
PRIOR FILING DATE: 1989-02-24
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 7
LENGTH: 1845
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein of B
NAME/KEY: CDS
LOCATION: (1) ..(1845)
OTHER INFORMATION:
US-10-102-469-7
Query Match 66.2%; Score 1845; DB 12; Length 1845;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1845; Conservative 0; Mismatches 0; Gaps 0;
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RESULT 2

; Sequence 5, Application US/09988462
; Publication No. US20030046726A1

APPLICANT: Koziel, Michael G

Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launus, Karen L.

```

1  TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE
2                      INSECTICIDAL ACTIVITY II
3
4  NUMBER OF SEQUENCES:  94
5
6  CORRESPONDENCE ADDRESS:
7
8  ADDRESSER: Syngenta Biotechnology, Inc
9
10 STREET: 3054 Cornwallis Road
11
12 CITY: Research Triangle Park

```

```

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY: misc feature
LOCATION: 1..1845
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1844; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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533 CCACCACGAGCAAGATTTCTCCACAGGTGAGCCACGCTGTCATGTTCCGTTCCGATTC 1320
534 |||||
535 CCACCACGAGCAAGATTTCTCCACAGGTGAGCCACGCTGTCATGTTCCGTTCCGATTC 1320
536 |||||
537 AGCAACAGTTCCGAGAGATCATCAGAGCTCTATGTTCTATGATTCATGCTAGTCT 1476
538 |||||
539 AGCAACAGTTCCGAGAGATCATCAGAGCTCTATGTTCTATGATTCATGCTAGTCT 1380
540 |||||
541 GAGTTCAACAATATCATCTTCTCTCAAAATCAACCAATCCATTGACCAAGTCTACT 1536
542 |||||
543 GAGTTCAACAATATCATCTTCTCTCAAAATCAACCAATCCATTGACCAAGTCTACT 1440
544 |||||
545 GAGTTCAACAATATCATCTTCTCTCAAAATCAACCAATCCATTGACCAAGTCTACT 1440

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Qy	1537	AACCTGGATCTGGAACTTCGTGTGTGAAAGACACAGGCTTCACAGGAGGATATCTT	1596
Db	1441	AACCTTGGATCTGGAACTTCGTGTGTGAAAGACACAGGCTTCACAGGAGGATATCTT	1500
Qy	1597	AGAGAACTTCTCTGTGGCAGATTAGCACTCTAGAGTTAACATCACTGCACCACTTCT	1656
Db	1501	AGAGAACTTCTCTGTGGCAGATTAGCACTCTAGAGTTAACATCACTGCACCACTTCT	1560
Qy	1657	CAAGATATCTGTGTACGAGTTCGTTACGCATCTACCACTTAACTTGCATTCACACCTCC	1716
Db	1561	CAAGATATCTGTGTACGAGTTCGTTACGCATCTACCACTTAACTTGCATTCACACCTCC	1620
Qy	1717	ATGACGGAAAGCCATATCAATCAGGGTAACCTTCCGCAACATGTCAGGGGACGAC	1776
Db	1621	ATGACGGAAAGCCATATCAATCAGGGTAACCTTCCGCAACATGTCAGGGGACGAC	1680
Qy	1777	TTGCAATCCGACAGCTTCAGAACCGTCGGTTTCACTACTCCTTTCAACTTCTCTAACGGA	1836
Db	1681	TTGCAATCCGACAGCTTCAGAACCGTCGGTTTCACTACTCCTTTCAACTTCTCTAACGGA	1740
Qy	1837	TCAAGCGTTTCACTCTTAAGCGTCACTATGTGTTCATTTCTGGCAATGAAGTATCAATTGAC	1896
Db	1741	TCAAGCGTTTCACTCTTAAGCGTCACTATGTGTTCATTTCTGGCAATGAAGTATCAATTGAC	1800
Qy	1897	CGATTTAGTGTGTGCTCGCCGGAAGTAACTTTCAGAGCTAGTAGTAC	1941
Db	1801	CGATTTAGTGTGTGCTCGCCGGAAGTAACTTTCAGAGCTAGTAGTAC	1845

RESULT 3
US-10-10

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: Sequence 23 Application US/10102469
: Publication No. US20030192078A1
:
: GENERAL INFORMATION:
:   APPLICANT: Fischhoff, David A.
:   APPLICANT: Petlak, Frederick J.
:   TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
:   FILE REFERENCE: 38-21 (13553) B
:   CURRENT APPLICATION NUMBER: US/10/102,469
:   CURRENT FILING DATE: 2002-09-05
:   PRIOR APPLICATION NUMBER: 08/434,105
:   PRIOR FILING DATE: 1995-05-03
:   PRIOR APPLICATION NUMBER: 07/959,506
:   PRIOR FILING DATE: 1992-10-09
:   PRIOR APPLICATION NUMBER: 07/476,661
:   PRIOR FILING DATE: 1990-02-12
:   PRIOR APPLICATION NUMBER: 07/315,355
:   PRIOR FILING DATE: 1989-02-24
:   NUMBER OF SEQ ID NOS: 43
:   SOFTWARE: PatentIn version 3.1
:   SEQ ID NO 23
:   LENGTH: 3531
:   TYPE: DNA
:   ORGANISM: artificial sequence
:   FEATURE:
:   OTHER INFORMATION: synthetic structural gene encoding a fusion protein derived from
:   OTHER INFORMATION: B.t.k. HD-1 and B.c.k. HD-73
:   FEATURE:
:   NAME/KEY: CDS
:   LOCATION: (1)..(3531)
:   OTHER INFORMATION:
:   US-102-469-23

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Query Match	66.1%	Score 1843.4	DB 12	Length 3531
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1844, Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY 97 ATGACAAACCAACCAATCAAGATTCATTCATCACTGTTGATACCCAGA 156

Db 1 ATGCACAACACCCAAATCATCAACAAATGCATTCATCACTGTTGATACCCAGA 60

QY 157 GTTGAAGTACTTGGTGAGAACGCATTGAACCGGTACATCCCATGACATCTCCCTTG 216

Db	61	GTTTAAAGTACTGGGTGGAGAAACGATGTAAACCGGTTAACACTCCCATCGACATCTCCGTTG	120
Qy	217	TCCTTGCACAGTTTCTGCTCAGGAGATTGTCGACAGTGTGGGTTGTTCTTGAGCTA	276
Db	121	TCCTTGGACAGATTTCGCTCAGGAGATTGGTGCAGAGTGTGGGTTCTGTTCTGGACTA	180
Qy	277	GTTGACATTCATCTGGGGTATCTTTGGTGCATCTCAATGGGATGCAATTCCTGGTCAATT	336
Db	181	GTTGACATTCATCTGGGGTATCTTTGGTGCATCTCAATGGGATGCAATTCCTGGTCAATT	240
Qy	337	GAGCAGTTGATTCACACGAGAGATCGAAGAGTTCCGCAAGAACCGGCCATCTTAGGTTG	396
Db	241	GAGCAGTTGATTCACACGAGAGATCGAAGAGTTGGCCAGAACGAGGCATCTTAGGTTG	300
Qy	397	GAAGAGTTGACCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGGAACCGCAT	456
Db	301	GAAGAGTTGACCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGGAACCGCAT	360
Qy	457	CCCTACTAACCCAGGCTCTCCGGAGAGAAATGGTATTTCAATTCAACGACATGAACGAGCC	516
Db	361	CCCTACTAACCCAGGCTCTCCGGAGAGAAATGGTATTTCAATTCAACGACATGAACGAGCC	420
Qy	517	TTGACCAAGCTATCCCATTTGTTGGACGTCCAGAACTACCAAGTTCCTCTTTCGGTG	576
Db	421	TTGACCAAGCTATCCCATTTGTTGGACGTCCAGAACTACCAAGTTCCTCTTTCGGTG	480
Qy	577	TACGTTCAAGCAGCTAACTCTTCACTCAGCGTGTCTGAGAGCTTTAGCGTTTGGGCAA	636
Db	481	TACGTTCAAGCAGCTAACTCTTCACTCAGCGTGTCTGAGAGCTTTAGCGTTTGGGCAA	540
Qy	637	AGGTGGGGATTCGATGCTGCAACCATTAATGACGGTTAACACGACCTTACTAGGCTGATT	696
Db	541	AGGTGGGGATTCGATGCTGCAACCATTAATGACGGTTAACACGACCTTACTAGGCTGATT	600
Qy	697	GGAAGTACTACACGACCAAGCTGTTGTTGGTACAAACTGCGCTTGGACGCTGTGGGGT	756
Db	601	GGAAGTACTACACGACCAAGCTGTTGTTGGTACAAACTGCGCTTGGACGCTGTGGGGT	660
Qy	757	CCTGATTTCTAGAGATTGATTTAGTATACAAACGATTCAGAGAGAAATGACCTTCAAGTT	816
Db	661	CCTGATTTCTAGAGATTGATTTAGTATACAAACGATTCAGAGAGAAATGACCTTCAAGTT	720
Qy	817	TTGACATTTGTGTCTCTCTTCCGAACTATGACTTCAGAACTTACCTATCCGTAAGTG	876
Db	721	TTGACATTTGTGTCTCTCTTCCGAACTATGACTTCAGAACTTACCTATCCGTAAGTG	780
Qy	877	TCCCAACTTACAGAGAAATCTATATCTAACCCAGTCTTGAGAACTTCGAGGGTAGCTTC	936
Db	781	TCCCAACTTACAGAGAAATCTATATCTAACCCAGTCTTGAGAACTTCGAGGGTAGCTTC	840
Qy	937	CGTGGTTCGCGCAAGGATCGAAGGCTCCATCAGAGGCCCACTTGATGAGACATCTTGG	996
Db	841	CGTGGTTCGCGCAAGGATCGAAGGCTCCATCAGAGGCCCACTTGATGAGACATCTTGG	900
Qy	997	AACAGCATATCTATCTTACACCGATGCTCACAGAGAGAGTATTACTGCTTCGACACGAG	1056
Db	901	AACAGCATATCTATCTTACACCGATGCTCACAGAGAGAGTATTACTGCTTCGACACGAG	960
Qy	1057	ATCATGGCTCTCCAGTTGGATTTAGGGGGGCCGAGTTTACCTTCCCTCTGATGGAAT	1116
Db	961	ATCATGGCTCTCCAGTTGGATTTAGGGGGGCCGAGTTTACCTTCCCTCTGATGGAAT	1024
Qy	1117	ATGGGAAACGCGCGTCCACAACAACTATCGTTGCTCAACTAGTCAAGGATGTCTACAGA	1176
Db	1021	ATGGGAAACGCGCGTCCACAACAACTATCGTTGCTCAACTAGTCAAGGATGTCTACAGA	1080
Qy	1177	ACCTTGTCTTCACTTGTATACAGAAAGCCTTCAATATCGGTATTAACAACACGACACTT	1233
Db	1081	ACCTTGTCTTCACTTGTATACAGAAAGCCTTCAATATCGGTATTAACAACACGACACTT	1140
Qy	1237	TCCGTTCTTGAAGGAAAGAGTGGCCATATGGAACCTTCTCAACTTGCATTCGCGCTGT	1296
Db	1141	TCCGTTCTTGAAGGAAAGAGTGGCCATATGGAACCTTCTTCAACTTGCATTCGCGCTGT	1200


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Db      901 AACAGCATATCTATCTACCCGATGCTCACAGAGAGATATCTAGTGTGACACCAG 960
Oy      1057 ATCATGCGCTCTCCAGTTGATGATTCAGCGGGCCCGAGTTTACCTTCTCTATGAACT 1116
Db      961 ATCATGCGCTCTCCAGTTGATGATTCAGCGGGCCCGAGTTTACCTTCTCTATGAACT 1020
Oy      1117 ATGGAAACGCCGCTCCACAAACGATCGTGTCTCACTAGTACAGGAGTGTCTACAGA 1176
Db      1021 ATGGAAACGCCGCTCCACAAACGATCGTGTCTCACTAGTACAGGAGTGTCTACAGA 1080
Oy      1177 ACCTTGCTTCCACCTTGTACAGAAAGCCCTCAATATCGGTATCAACACAGCAACTT 1236
Db      1081 ACCTTGCTTCCACCTTGTACAGAAAGCCCTCAATATCGGTATCAACACAGCAACTT 1140
Oy      1237 TCCGTTCTTTCAGCAACAGAGTTCCGCTATGAAACCTCTTCACTTCCATCCGCTGT 1296
Db      1141 TCCGTTCTTTCAGCAACAGAGTTCCGCTATGAAACCTCTTCACTTCCATCCGCTGT 1200
Oy      1297 TACAGAAAGACCGGAACCGTTGATTCCTTGAACGAATCCCAACAGAAACAAATGTG 1356
Db      1201 TACAGAAAGACCGGAACCGTTGATTCCTTGAACGAATCCCAACAGAAACAAATGTG 1260
Oy      1357 CCACCCAGGCAAGATTTCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGATTC 1416
Db      1261 CCACCCAGGCAAGATTTCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGATTC 1320
Oy      1417 AGCAACGTTCCGAGAGCATCATCAGAGTCTCTATGTTCTCATGATCATCGTAGTCT 1476
Db      1321 AGCAACGTTCCGAGAGCATCATCAGAGTCTCTATGTTCTCTGATACACCGTAGTCT 1380
Oy      1477 GAGTTCAACAAATATCATTCCTTCTCTGTAATCACCACCAATCCCAATGCAAGTCTACT 1536
Db      1381 GAGTTCAACAAATATCATTCGATTCGATAGTATTAATCCCTGCAAGTGAAG---GGA 1437
Oy      1537 AACCTTGATCTGGAACCTTCTGTGCGTGAAGAACCAAGCTTACAGAGAGTATTTCTT 1596
Db      1438 AACCTTCTCTCAACGAGTTCTGTCAATTCAGAGACAGAGATTCATGCTGAGAGCTCTGT 1497
Oy      1597 AGA 1599
Db      1498 AGA 1500

RESULT 5
US-10-102-469-9
; Sequence 9, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; APPLICANT: Petlak, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein derive
; NAME/KEY: CDS

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; LOCATION: (1)..(3534)
; OTHER INFORMATION:
US-10-102-469-9
Query Match      50.6%; Score 1411.8; DB 12; Length 3534;
Best local similarity 96.7%; Pred. No. 0;
Matches 1453; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

Oy      97  ATGACAAACAAACCCAAACATCAAGAAATGCAATTCATACAACTGCTTGAGTAACCCAGAA 156
Db      1  ATGACAAACAAACCCAAACATCAAGAAATGCAATTCATACAACTGCTTGAGTAACCCAGAA 60
Oy      157  GTTGAAGTACTTGTGGTGAAGAACGATTTGAACCCGTTACATCTCCCATGACATCTCTTG 216
Db      61  GTTGAAGTACTTGTGGTGAAGAACGATTTGAACCCGTTACATCTCCCATGACATCTCTTG 120
Oy      217  TCCTTGACAGAGTTTCTGCTCAGGAGAGTGTGTCAGAGTGTGAGGTTGCTTCTCGGACTA 276
Db      121  TCCTTGACAGAGTTTCTGCTCAGGAGAGTGTGTCAGAGTGTGAGGTTGCTTCTCGGACTA 180
Oy      277  GTTGACATCATCTGCGGATATCTTTGTCATCTCAATGGAGATGCAATTCCTGATGCAAAAT 336
Db      181  GTTGACATCATCTGCGGATATCTTTGTCATCTCAATGGAGATGCAATTCCTGATGCAAAAT 240
Oy      337  GAGCAGTTGATCAACACAGAGATCGAAGAGTTCCGACAGAACACAGGCCATCTTATGTTG 396
Db      241  GAGCAGTTGATCAACACAGAGATCGAAGAGTTCCGACAGAACACAGGCCATCTTATGTTG 300
Oy      397  GAAAGATGACCAATCTCTACCAAAATCTATGACAGAGCTTCAGAGATGGGGAAGCCGAT 456
Db      301  GAAAGATGACCAATCTCTACCAAAATCTATGACAGAGCTTCAGAGATGGGGAAGCCGAT 360
Oy      457  CCTACTAACCCAGCTCTCCGAGAGAAATGCGTATTCATTCACAGCATGAACAGCGCC 516
Db      361  CCTACTAACCCAGCTCTCCGAGAGAAATGCGTATTCATTCACAGCATGAACAGCGCC 420
Oy      517  TTGACCAACAGCTATCCCATTTGTTGCGAGTCCAGAACTACAGAGTTCTCTTGTCCGTG 576
Db      421  TTGACCAACAGCTATCCCATTTGTTGCGAGTCCAGAACTACAGAGTTCTCTTGTCCGTG 480
Oy      577  TACGTTCAAGAGAGCAATCTTCACTCAGCGGCTTCGAGAGAGTTAGCGTGTGTTGGGCA 636
Db      481  TACGTTCAAGAGAGCAATCTTCACTCAGCGGCTTCGAGAGAGTTAGCGTGTGTTGGGCA 540
Oy      637  AGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTACACAGACCTTACTAGGCTGAT 696
Db      541  AGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTACACAGACCTTACTAGGCTGAT 600
Oy      697  GGAACCTACACCGACACGCTGTTGTTGTTGTAACAACACTGCTTGGAGCGTGTGGGGT 756
Db      601  GGAACCTACACCGACACGCTGTTGTTGTTGTAACAACACTGCTTGGAGCGTGTGGGGT 660
Oy      757  CCTGATTCAGAGATTGGAATTAGATACAAACGATTCAAGAGAAATTGACCTCCACAGTT 816
Db      661  CCTGATTCAGAGATTGGAATTAGATACAAACGATTCAAGAGAAATTGACCTCCACAGTT 720
Oy      817  TTGACATTTGTCTCTCTTCCGAACTATGACTCCAGAACCTTACCTATCCGTAAGTG 876
Db      721  TTGACATTTGTCTCTCTTCCGAACTATGACTCCAGAACCTTACCTATCCGTAAGTG 780
Oy      877  TCCCAACTTACAGAGAAATCTATCTAACCCAGTTCTTGAGAACTTGCACGCTGACTTC 936
Db      781  TCCCAACTTACAGAGAAATCTATCTAACCCAGTTCTTGAGAACTTGCACGCTGACTTC 840
Oy      937  CGTGGTTGACCAAGGATGGAAGGCTCATCAGAGCCACACTTGTGATGACATCTTG 996
Db      841  CGTGGTTGACCAAGGATGGAAGGCTCATCAGAGCCACACTTGTGATGACATCTTG 900
Oy      997  AACAGCATATATCTATACACCGATGCTCAACAGAGAGATATTAAGTGTGACACAG 1056
Db      901  AACAGCATATATCTATACACCGATGCTCAACAGAGAGATATTAAGTGTGACACAG 960
Oy      1057  ATCATGCGCTCTCCAGTTGATGATTCAGCGGGCCCGAGTTTACCTTCTCTATGAACT 1116

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Db      ATCATGGGCTCTCCAGTTGGATTCAAGCGGGCCAGATTACCTTCCCTCTATGAACT 1020
Qy      1117 ATGGAAAGCGCGCTCCCAACAACGATCGTGTCAACTAAGGTCAGGGGTCTACAGA 1176
Db      1021 ATGGAAAGCGCGCTCCCAACAACGATCGTGTCAACTAAGGTCAGGGGTCTACAGA 1080
Qy      1177 ACCTTGCTCTCCACCTTGATACAGAAAGCCCTTCAATCGGTATCAACAACAGCAACTT 1236
Db      1081 ACCTTGCTCTCCACCTTGATACAGAAAGCCCTTCAATCGGTATCAACAACAGCAACTT 1140
Qy      1237 TCCGTTCTTGAACGAAACAGAGTTGGCTATGAAACCTCTTAACTTCCATCCGCTGT 1236
Db      1141 TCCGTTCTTGAACGAAACAGAGTTGGCTATGAAACCTCTTAACTTCCATCCGCTGT 1200
Qy      1297 TACGAAAGAGCGGAACCGTGTGATTCCTGTGACGAAATCCACACAGAAACAACATGTG 1356
Db      1201 TACGAAAGAGCGGAACCGTGTGATTCCTGTGACGAAATCCACACAGAAACAACATGTG 1260
Qy      1357 CCACCCAGGCAAGATTCCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGATTC 1416
Db      1261 CCACCCAGGCAAGATTCCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGATTC 1320
Qy      1417 AGCAACAGTTCGAGAGCATCATCAGAGCTCTATGTTCTCATGAGATTCAATGAGTCT 1476
Db      1321 AGCAACAGTTCGAGAGCATCATCAGAGCTCTATGTTCTCTGTGATTACACCGTAGTCT 1380
Qy      1477 GAGTTCAACAATATCATTCCTTCCCTCAATTCACCAATCCCATTTGACCAAGCTACT 1536
Db      1381 GAGTTCAACAATATCATTCCTTCCCTCAATTCACCAATCCCATTTGACCAAGCTACT 1437
Qy      1537 AACCTTGATCTGAAACTTCTGTCGTGAAAGAACAGGCTTACAGAGAGTGATATTTT 1596
Db      1438 AACCTTCTCTTCAACGAGTTCTGTGATTCATTCAGAGACAGAGTTCAGTGTGAGACTCTGTT 1497
Qy      1597 AGA 1599
Db      1498 AGA 1500

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RESULT 6

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US-10-102-469-11
; Sequence 11, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; APPLICANT: Perlak, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein derivative
; NAME/KEY: CDS
; LOCATION: (1)..(3534)
; OTHER INFORMATION:
US-10-102-469-11

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Query Match 50.6%; Score 1411.8; DB 12; Length 3534;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1453; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
Qy      97 ATGACAAACAACCCAAACATCAACGATTCATCAACAACTGCTGAGTAACCCAGAA 156
Db      1 ATGACAAACAACCCAAACATCAACGATTCATCAACAACTGCTGAGTAACCCAGAA 60
Qy      157 GTTGAATGACTGGTGGAGAAACGATGAAACCGGTTACACTCCCATCGACATCTCTTG 216
Db      61 GTTGAATGACTGGTGGAGAAACGATGAAACCGGTTACACTCCCATCGACATCTCTTG 120
Qy      217 TCCCTTGAACAGATTTCCTCAGCAGGTTCTGTCAGAGTCTGAGGTTCTTCTGCACTA 276
Db      121 TCCCTTGAACAGATTTCCTCAGCAGGTTCTGTCAGAGTCTGAGGTTCTTCTGCACTA 180
Qy      277 GTTGAATCATCTGGGATTCCTTGTGTCATCTCAATGGAGTGCATTCCTGTGTCAATT 336
Db      181 GTTGAATCATCTGGGATTCCTTGTGTCATCTCAATGGAGTGCATTCCTGTGTCAATT 240
Qy      337 GAGCAGTTGATCAACACAGAGATGGAAGATTCGCCAGAAACAGCCATCTTAGGTTG 396
Db      241 GAGCAGTTGATCAACACAGAGATGGAAGATTCGCCAGAAACAGCCATCTTAGGTTG 300
Qy      397 GAAAGATTGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGAAACCGAT 456
Db      301 GAAAGATTGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGAAACCGAT 360
Qy      457 CCTACTAACCAGCTCTCCCGAGAGAAATGGTATTCATCAACAGCATGAACAGGCC 516
Db      361 CCTACTAACCAGCTCTCCCGAGAGAAATGGTATTCATCAACAGCATGAACAGGCC 420
Qy      517 TTGACCAAGCTATCCCATTTGTTGAGTCAGATCCAGAACTACCAAGTTCCTCTTCTG 576
Db      421 TTGACCAAGCTATCCCATTTGTTGAGTCAGATCCAGAACTACCAAGTTCCTCTTCTG 480
Qy      577 TAGGTTCAAGAGCTAATCTTCACTCAGCGTCTTGAGAGCTTACGCTGTTGGCA 636
Db      481 TAGGTTCAAGAGCTAATCTTCACTCAGCGTCTTGAGAGCTTACGCTGTTGGCA 540
Qy      637 AGGTGGGATTCGATTCGTGCAACCATTAAGCCGTACACAGACCTTACAGCTGAT 696
Db      541 AGGTGGGATTCGATTCGTGCAACCATTAAGCCGTACACAGACCTTACAGCTGAT 600
Qy      697 GGAACATCAACGACGACGAGCTGTTGTTGTAACAACACTGCTGAGACGTCGTGGGT 756
Db      601 GGAACATCAACGACGACGAGCTGTTGTTGTAACAACACTGCTGAGACGTCGTGGGT 660
Qy      757 CCTGATCTAGAGATTGGATTAGATACCAACGATTCAGAGAGATTGACCTCTACAGTT 816
Db      661 CCTGATCTAGAGATTGGATTAGATACCAACGATTCAGAGAGATTGACCTCTACAGTT 720
Qy      817 TTGACATTTGCTCTCTTCCCAACATGACCTCCAGAACCTACCTATCCGTACAGT 876
Db      721 TTGACATTTGCTCTCTTCCCAACATGACCTCCAGAACCTACCTATCCGTACAGT 780
Qy      877 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCCTTGAACCTTGAACCTTGAAGCTTC 936
Db      781 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCCTTGAACCTTGAAGCTTGAAGCTTC 840
Qy      937 CGTGCTTCCCAAGGATTCGAAAGCTTCATCAGAGCCCACTTATGATGACATCTTG 996
Db      841 CGTGCTTCCCAAGGATTCGAAAGCTTCATCAGAGCCCACTTATGATGACATCTTG 900
Qy      997 AACGCAATATCATATTAACGAGTCTCAGAGAGAGATTAATGAGTCTGACACAG 1056
Db      901 AACGCAATATCATATTAACGAGTCTCAGAGAGAGATTAATGAGTCTGACACAG 960
Qy      1057 ATCATGGCTCTCCAGTTGAGATTCAAGCGGCCGAGATTACCTTCTCTATGAACT 1116
Db      961 ATCATGGCTCTCCAGTTGAGATTCAAGCGGCCGAGATTACCTTCTCTATGAACT 1020

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Oy	1117	TTGGAAACGCGCTCCACAACAACGATTCGTGGTCAACATAGGTCAGGGGTCTACAGA	1176
Db	1021	ATGGAAACGCGCTCCACAACAACGATTCGTGGTCAACATAGGTCAGGGGTCTACAGA	1080
Oy	1177	ACCTGTCTTCACTGTGTACAGAAGACCTTCAATATCGGTATCAACACAGCAACTT	1236
Db	1081	ACCTGTCTTCACTGTGTACAGAAGACCTTCAATATCGGTATCAACACAGCAACTT	1140
Oy	1237	TCCGTTCTTGAACGAAAGAGTGGCCATAGAAACCTTGTAACTTGGCATCCGCTGT	1296
Db	1141	TCCGTTCTTGAACGAAAGAGTGGCCATAGAAACCTTGTAACTTGGCATCCGCTGT	1200
Oy	1297	TACAGAAAGACGGAAACCGTTGATTCCTTGAACGAATCCACACACAGAACAAATGTG	1356
Db	1201	TACAGAAAGACGGAAACCGTTGATTCCTTGAACGAATCCACACACAGAACAAATGTG	1260
Oy	1357	CCACCGACGGCAAGATTCTCCACACAGTTGAGCCACGTTGCATGTTCCGTCGGGATTC	1416
Db	1261	CCACCGACGGCAAGATTCTCCACACAGTTGAGCCACGTTGCATGTTCCGTCGGGATTC	1320
Oy	1417	AGCAACAGTTCGTGAGCATCATCAGAGCTCCTATGTTCTGATGATTCATCGTAGTCT	1476
Db	1321	AGCAACAGTTCGTGAGCATCATCAGAGCTCCTATGTTCTGATGATTCATCGTAGTCT	1380
Oy	1477	GAGTTCAACATATCATCTTCTCTCTCAATTCACCCCAAAATCCCATTTGACCAAGTCACT	1536
Db	1381	GAGTTCAACATATCATCTTCTCTCTCAATTCACCCCAAAATCCCATTTGACCAAGTCACT	1437
Oy	1537	AACCTTGATCTGAACTTCTGTGTAAGAGACCGAGCTTCACAGAGGTGATATTCCT	1596
Db	1438	AACCTTGATCTGAACTTCTGTGTAAGAGACCGAGCTTCACAGAGGTGATATTCCT	1497
Oy	1597	AGA 1599	
Db	1498	AGA 1500	

RESULT 7
US-10-102-469-13
; Sequence 13, Application US/10102469
; Publication No. US20030192078A1

GENERAL INFORMATION:
 APPLICANT: Fischhoff, David A.
 APPLICANT: Perlak, Frederick J.
 TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
 FILE REFERENCE: 38-21 (1355) B
 CURRENT APPLICATION NUMBER: US/10/102,469
 CURRENT FILING DATE: 2002-09-05
 PRIOR APPLICATION NUMBER: 08/434,105
 PRIOR FILING DATE: 1995-05-03
 PRIOR APPLICATION NUMBER: 07/959,506
 PRIOR FILING DATE: 1992-10-09
 PRIOR APPLICATION NUMBER: 07/476,661
 PRIOR FILING DATE: 1990-02-12
 PRIOR APPLICATION NUMBER: 07/315,355
 PRIOR FILING DATE: 1989-02-24
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1

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/ SEQ_ID: NO. 13
/ LENGTH: 3534
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein derivative
/ FEATURE:
/ OTHER INFORMATION: d from B.t.k. HD-73
/ NAME/KEY: CDS
/ LOCATION: (1)..(3534)
/ OTHER INFORMATION:
US-10-102-469-13

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Query Match	50.6%;	Score 1411.8;	DB 12;	Length 3534;
Best Local Similarity	96.7%;	Pred. No. 0;		

Matches 1453; Conservative 0; Mismatches 47; Indels 3; Gaps 1,	
QY	97 ATGACAAACAACCCAAACATCAACGAATGCATTCCTACACAACTGCTTGAGTAAACCCGAA 156
Db	1 ATGACAAACAACCCAAACATCAACGAATGCATTCCTACACAACTGCTTGAGTAAACCCGAA 60
QY	157 GTTGAAGTACTCTGTGTGGAGAACGATGGAACCGGTGACCTCCATCGACATCTCTCTG 216
Db	61 GTTGAAGTACTCTGTGTGGAGAACGATGGAACCGGTGACCTCCATCGACATCTCTCTG 120
QY	217 TCCTTGACACAGTTTCTGCTCAGGAGTTGCTGCGACGTCGTGGTTCGTTCTGACATA 276
Db	121 TCCTTGACACAGTTTCTGCTCAGGAGTTGCTGCGACGTCGTGGTTCGTTCTGACATA 180
QY	277 GTTGAACATCATCTGGGGTATCTTTGGTTCATCTCAATGGAGTGCATTCCTGTGTCAATT 336
Db	181 GTTGAACATCATCTGGGGTATCTTTGGTTCATCTCAATGGAGTGCATTCCTGTGTCAATT 240
QY	337 GAGCAGTTGATCAACGAGAGATCGAAGAGTGGCCGAGAACCGAGCATCTCTAGGTG 396
Db	241 GAGCAGTTGATCAACGAGAGATCGAAGAGTGGCCGAGAACCGAGCATCTCTAGGTG 300
QY	397 GAAGATTTGACATCTCTACCAATCTATGCAAGAGCTTCAGAGATGGGAAAGCCGAT 456
Db	301 GAAGATTTGACATCTCTACCAATCTATGCAAGAGCTTCAGAGATGGGAAAGCCGAT 360
QY	457 CCTACTAACCCAGCTCTCCGCGAGAGAAATGGCTATTCAATTCAACGACATGACAGGCC 516
Db	361 CCTACTAACCCAGCTCTCCGCGAGAGAAATGGCTATTCAATTCAACGACATGACAGGCC 420
QY	517 TTGACCAACAGTATCCCATTTGGAGTCCAGATCCAGAACTACAAAGTTCCTCTCTGTCGGT 576
Db	421 TTGACCAACAGTATCCCATTTGGAGTCCAGATCCAGAACTACAAAGTTCCTCTCTGTCGGT 480
QY	577 TACGTTCAACAGCTAATCTTCAACCTCAGCGTCTTGAGAGCGTTAGCGTGTGGCGAA 636
Db	481 TACGTTCAACAGCTAATCTTCAACCTCAGCGTCTTGAGAGCGTTAGCGTGTGGCGAA 540
QY	637 AGGTGGGGAATTCGATGCTGCAACCATCATATGCCGTTACCAAGACTTACTAGCTGATT 696
Db	541 AGGTGGGGAATTCGATGCTGCAACCATCATATGCCGTTACCAAGACTTACTAGCTGATT 600
QY	697 GGAACCTACACCCGACACGCTGTCGTTGGTATCAACACTGGCTTGAGCGGTCTGGGGT 756
Db	601 GGAACCTACACCCGACACGCTGTCGTTGGTATCAACACTGGCTTGAGCGGTCTGGGGT 660
QY	757 CCTGATTCCTAGAGATTTGGATTAGTACAACGATTCAGAGAGAAATGACCTCACAAGTT 816
Db	661 CCTGATTCCTAGAGATTTGGATTAGTACAACGATTCAGAGAGAAATGACCTCACAAGTT 720
QY	817 TTGACATTTGTGTCTCTTCCCGAATATGACTCCAGAACCTTACCTATCGTACAGTG 876
Db	721 TTGACATTTGTGTCTCTTCCCGAATATGACTCCAGAACCTTACCTATCGTACAGTG 780
QY	877 TCCCAACTTACCAAGAGAAATCTATACCTAACCCGATTTCTTGAGAACTTCGAGGTAAGCTTC 936
Db	781 TCCCAACTTACCAAGAGAAATCTATACCTAACCCGATTTCTTGAGAACTTCGAGGTAAGCTTC 840
QY	937 CGTGGTTCGCGCAAGGATCGAAGGCTCCATCAGAGAGCCCACTTGATGGAATCTTGG 996
Db	841 CGTGGTTCGCGCAAGGATCGAAGGCTCCATCAGAGAGCCCACTTGATGGAATCTTGG 900
QY	997 AACGACATAACTATCTACACCGATGCTCACAGAGAGATTAATCTGCTCGACACCGAG 1056
Db	901 AACGACATAACTATCTACACCGATGCTCACAGAGAGATTAATCTGCTCGACACCGAG 960
QY	1057 ATCATGGCTCTCCAGTTGGATTTAGGGGGCCGAGTTTACCTTTCTCTCTATGGAATCT 1116
Db	961 ATCATGGCTCTCTCCAGTTGGATTTAGGGGGCCGAGTTTACCTTTCTCTCTATGGAATCT 1020
QY	1117 ATGGGAAACGGCGCTCCACAACAGATATGCTTCTCAATAGGTCAGGGGTCTTACAGAA 1176
Db	1021 ATGGGAAACGGCGCTCCACAACAGATATGCTTCTCAATAGGTCAGGGGTCTTACAGAA 1080

QY 1177 ACCTGTCTTCACCTGTGTACAGAGACCCCTTCAATATCGGTATCAACACCAACTT 1236
 Db 1081 ACCTGTCTTCACCTGTGTACAGAGACCCCTTCAATATCGGTATCAACACCAACTT 1140
 QY 1237 TCCGTTCTTGACGGAACGAGTGGCCCTATGGAACCTCTTAACTTCCATCCGCTGT 1236
 Db 1141 TCCGTTCTTGACGGAACGAGTGGCCCTATGGAACCTCTTAACTTCCATCCGCTGT 1200
 QY 1297 TACAGAAAGACGGGACCGGTGATTCCTTGACGGAATCCACACAGAAACAATGTG 1356
 Db 1201 TACAGAAAGACGGGACCGGTGATTCCTTGACGGAATCCACACAGAAACAATGTG 1280
 QY 1357 CCACCCAGGCAAGGATTCCTCCACAGGTGAGCCAGTGTCCATGTTCCGTTCCGATTC 1416
 Db 1261 CCACCCAGGCAAGGATTCCTCCACAGGTGAGCCAGTGTCCATGTTCCGTTCCGATTC 1320
 QY 1417 AGCAACAGTTCCTGTAGAGATCATGAGACTCTCTAATGTTCTCATGATTCATCTGATGCT 1476
 Db 1321 AGCAACAGTTCCTGTAGAGATCATGAGACTCTCTAATGTTCTCATGATTCATCTGATGCT 1380
 QY 1477 GAGTTCAACAATATCATCTCTCTCTCAATACCAATCCCAATCCCATGACCAAGTCTACT 1536
 Db 1381 GAGTTCAACAATATCATCTCTCTCTCAATACCAATCCCAATCCCATGACCAAGTCTACT 1437
 QY 1537 AACCTTGATCTGGAACCTTCTGTCTGGAAGAGACCGGCTTCACAGAGGTGATATCTT 1596
 Db 1438 AACCTTCTCTTCAACGGTTCTGTCTGATTCAGAGACGAGATTCACTGTGTGAGACTCTGTT 1497
 QY 1597 AGA 1599
 Db 1498 AGA 1500
 RESULT 8
 US-10-102-469-5
 ; Sequence 5, Application US/10102469
 ; Publication No. US20030192078A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischhoff, David A.
 ; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
 ; FILE REFERENCE: 38-21 (13553) B
 ; CURRENT APPLICATION NUMBER: US/10/102,469
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: 08/434,105
 ; PRIOR FILING DATE: 1995-05-03
 ; PRIOR APPLICATION NUMBER: 07/959,506
 ; PRIOR FILING DATE: 1992-10-09
 ; PRIOR APPLICATION NUMBER: 07/476,661
 ; PRIOR FILING DATE: 1990-02-12
 ; PRIOR APPLICATION NUMBER: 07/315,355
 ; PRIOR FILING DATE: 1989-02-24
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 1767
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein derive
 ; OTHER INFORMATION: d from B.t.k. HD-73
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1767)
 ; OTHER INFORMATION:
 US-10-102-469-5
 Query Match 47.7%; Score 1328.8; DB 12; Length 1767;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 1370; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
 QY 180 CATTGAACCGGTACACTCCATGCATCATCTTCCTTGTCTTGACACAGTTTCTGTGACG 239

Db 6 CATTGAACCGGTACACTCCATGCATCATCTTCCTTGTCTTGACACAGTTTCTGTGACG 65
 QY 240 CGAGTTGTCGACAGTGTCTGGTTCGTTCTCGAGCTAGTATCATCTGTGGGATCTT 299
 Db 66 CGAGTTGTCGACAGTGTCTGGTTCGTTCTCGAGCTAGTATCATCTGTGGGATCTT 125
 QY 300 TGGTCCATCTCAATGAGATGATCTCTGTGTGCAATTTAGCAAGTTGATCAACAGAGAT 359
 Db 126 TGGTCCATCTCAATGAGATGATCTCTGTGTGCAATTTAGCAAGTTGATCAACAGAGAT 185
 QY 360 CGAAGATTTGCCAGAGAACAGGCAATCTCTAGTTGGAAGGATTTGAGCAATCTTCA 419
 Db 186 CGAAGATTTGCCAGAGAACAGGCAATCTCTAGTTGGAAGGATTTGAGCAATCTTCA 245
 QY 420 AATCTATGACAGAGACTTTCAGAGAGTGGGAAGCCGATCTCTAATACCAGCTTCCGGA 479
 Db 246 AATCTATGACAGAGACTTTCAGAGAGTGGGAAGCCGATCTCTAATACCAGCTTCCGGA 305
 QY 480 GGAATGCGTATTCATTAATTCACGATGAACAGCGCTTGAACACAGCTATCCATTTGT 539
 Db 306 GGAATGCGTATTCATTAATTCACGATGAACAGCGCTTGAACACAGCTATCCATTTGT 365
 QY 540 CGCAGTCCAGAACTACCAAGTCTCTCTGTCGCTGTAGCTTCAAGCAGTATCTTCA 599
 Db 366 CGCAGTCCAGAACTACCAAGTCTCTCTGTCGCTGTAGCTTCAAGCAGTATCTTCA 425
 QY 600 CCTCAGCGTCTTGCAGAGCTTACGCTGTTTGGGCAAGGTGGGATTCGATGTGTGCAAC 659
 Db 426 CCTCAGCGTCTTGCAGAGCTTACGCTGTTTGGGCAAGGTGGGATTCGATGTGTGCAAC 485
 QY 660 CATCAATAGCCGTTTACACGACCTTACTAGGCTGATTTGAAATTCACACCGACGCTGT 719
 Db 486 CATCAATAGCCGTTTACACGACCTTACTAGGCTGATTTGAAATTCACACCGACGCTGT 545
 QY 720 TCGTTGGTACAAACCTGGCTTGGAGCGTGTGGGGTCTCGAATCTGAGATTGAGATTG 779
 Db 546 TCGTTGGTACAAACCTGGCTTGGAGCGTGTGGGGTCTCGAATCTGAGATTGAGATTG 605
 QY 780 ATACAAACAGTTCAGAGAGAGATTAACCTTACAGTTTGGACAATGTGTCTCTTCCC 839
 Db 606 ATACAAACAGTTCAGAGAGAGATTAACCTTACAGTTTGGACAATGTGTCTCTTCCC 665
 QY 840 GAACTATGACTTCCGAACCTTACCTTATCCGTACAGTGTCCCACTTACAGAGAAATTTA 899
 Db 666 GAACTATGACTTCCGAACCTTACCTTATCCGTACAGTGTCCCACTTACAGAGAAATTTA 725
 QY 900 TACTAACCCAGTTCGTAGAACTTGAACGAGTTCGAGTTCGAGTTCGAGGATTTGGA 959
 Db 726 TACTAACCCAGTTCGTAGAACTTGAACGAGTTCGAGTTCGAGTTCGAGGATTTGGA 785
 QY 960 AGGCTCCATCAGAGACCCACACTTATGATGATGATCTTGAACAGCATTAATCTATCACCGA 1019
 Db 786 AGGCTCCATCAGAGACCCACACTTATGATGATGATCTTGAACAGCATTAATCTATCACCGA 845
 QY 1020 TGGTCAAGAGAGAGATTAATCTGAGTGTGACACCAAGATCATGAGCTTCCAGTTGATT 1079
 Db 846 TGGTCAAGAGAGAGATTAATCTGAGTGTGACACCAAGATCATGAGCTTCCAGTTGATT 905
 QY 1080 CAGGGGGGCGAGTTTACCTTCCCTCTATGAACTATGGAAGGAGGAGGCTCCACACA 1139
 Db 906 CAGGGGGGCGAGTTTACCTTCCCTCTATGAACTATGGAAGGAGGAGGCTCCACACA 965
 QY 1140 ACGTATCGTCTCAACTAGGTGAGGTGTCTACAGAACTTGTCTTCCACTGTGTACAG- 1199
 Db 966 ACGTATCGTCTCAACTAGGTGAGGTGTCTACAGAACTTGTCTTCCACTGTGTACAG- 1025
 QY 1200 AAGACCTTCAATATCGGTATCAACACAGCACTTCCGTTCTTGACGGAACAGATT 1259
 Db 1026 AAGACCTTCAATATCGGTATCAACACAGCACTTCCGTTCTTGACGGAACAGATT 1085
 QY 1260 CGCCTATGAAACCTTCTTAACCTTGCATCGCTGTGTTACAGAAAGACGGAACGCTTGA 1319

Db 1086 GCGCTATGGAACCTCTTTCTTAACCTTGCCATCCGCTGTTTACAGAAAAGCGGAACCGTTGA 1145
Qy 1320 TTCCTTGGACGAAATCCCAACCAAGAACATATGTGCAACCCAGGACGAGATTTCTCCCA 1379
Db 1146 TTCCTTGGACGAAATCCCAACCAAGAACATATGTGCAACCCAGGACGAGATTTCTCCCA 1205
Qy 1380 CAGGTGAGCCACGCTGCTTCCATGTTCCGTTCCGATTCAGCAACAGTTCCGTGAGCATCAT 1439
Db 1206 CAGGTGAGCCACGCTGCTTCCATGTTCCGTTCCGATTCAGCAACAGTTCCGTGAGCATCAT 1265
Qy 1440 CAGAGCTCCTATGTTCTCATGATTCATGCTGAGTCCGATTCGAAATATCATTTCTCTTC 1499
Db 1266 CAGAGCTCCTATGTTCTCTTGAATACCGTAGTGTGATTCAGCAACATCATGCAATC 1325
Qy 1500 CTCCTAATCACCAGAAATCCCATTTGACCAAGTCTACTAACCCTTGATCTGGAATCTTGT 1559
Db 1326 CGATAGTATTTACTCAAAATCCCTGCAAGTGAAG---GGAATCTTCTCTTCAACGGTTCTGT 1382
Qy 1560 CGTGAAAGACCAAGGCTTCACAGAGGTGATATTCTTGA 1599
Db 1383 CATTTCAAGACCAAGGATTCACCTGTGTGAGACCTCGTTAGA 1422

RESULT 9
US-09-756-643-1
; Sequence 1, Application US/09756643
; Patent No. US20010026939A1
; GENERAL INFORMATION:
; APPLICANT: Rice, Douglas
; APPLICANT: Carozzi, Nadine
; APPLICANT: Anderson, David
; APPLICANT: Rajasekaran, Kanniah
; APPLICANT: Rangan, Thirumale
; APPLICANT: Yenofsky, Richard
; APPLICANT: Lotstein, Richard
; APPLICANT: De Pramond, Annick
; TITLE OF INVENTION: Insecticidal Cotton Plant Cells
; FILE REFERENCE: S-16768E
; CURRENT APPLICATION NUMBER: US/09/756,643
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 08/218,697
; PRIOR FILING DATE: 1994-03-28
; PRIOR APPLICATION NUMBER: 07/759,969
; PRIOR FILING DATE: 1991-09-16
; PRIOR APPLICATION NUMBER: 07/274,452
; PRIOR FILING DATE: 1988-11-18
; PRIOR APPLICATION NUMBER: 07/122,109
; PRIOR FILING DATE: 1987-11-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4360
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(3623)
US-09-756-643-1

Query Match 43.8%; Score 1220.4; DB 9; Length 4360;
Best Local Similarity 77.6%; Freq. No. 0;
Matches 1476; Conservative 0; Mismatches 426; Indels 0; Gaps 0;

Qy 39 AAAAAAAGCTTAATATTCGAGATTATTCATACCGTCCACCATCGGCGCGAGTCAAT 98
Db 98 AAAAAAGATATATATCATATGATGTTGTATCTTAATAAAGATGAGTAACTTAT 157
Qy 99 GGACAAACAAACCAACATCAACGAATGATTCATCAACAATGCTTGAGTAACCAAGAT 158
Db 158 GGATTAACATCCGAACATCAATGAATGATTCCTTAATATGTTTAAAGTAACCTGAAGT 217
Qy 159 TGAATACCTGTGTGAGAAAGCATTGAACCGGTTAACTCCCATGACATCTCCCTGTC 218

Db 218 AGAAGTATTAGTGGAGAAAAGATAGAAACTGGTTACACCCCAATGCATATTCTCTGTC 277
Qy 219 CTGACACAGATTTCTGCTCAGCGATTGCGCCAGGTGCTGGGTTCTCTCGAGTAGT 278
Db 278 GCTAACCAATTTCTTTGAGTGAATTTGTTCCCGGTGCTGAGATTTGTGTAGAGACTAGT 337
Qy 279 TGACATATCTGGGGTATCTTTGGTCCATCTCAATGGGATGCAATTCCTGGTGCAATTTGA 338
Db 338 TGATATATATATGGGGAATTTTGGTCTCCCTCATAGGGAACGCAATTTCTTGACAAATTTGA 397
Qy 339 GCAGTTATATCAACGAGAGATTCGAAGATTGCGCAGGAACCAAGGSCATCTCTAGTTGGA 398
Db 398 ACAGTTATATTAACCAAGAAATAGAAAGATTGCTAGGAACCAAGCAATTTCTAGATTAGA 457
Qy 399 AGGATGAGCAATCTCTACCAATCTATGCAAGAGCTTCAGAGAGTGGAGAGCCGATCC 458
Db 458 AGGACTAAGCAATCTTTATCAAAATTTAGCGAATCTTTTAGAAGTGGGAAGCAGATTC 517
Qy 459 TACTAACCCAGCTCTCCGCGAAGAAATGCGTATTCAATTCAACGACATGAACAGCGCTT 518
Db 518 TACTAATCCAGCATTAAGAGAGATGCGGATTCATTCATGACATGAACAGTGCCT 577
Qy 519 GACCAGACTATCCATTTGTTGCGAGTCCAGAACTTACCAAGTTCTCTGTGTCGATGA 578
Db 578 TACAACCGCTATTTCTCTTTTTCGAGTTCAAAATTAACAGTTCTCTTTTATCAGTATA 637
Qy 579 CGTTCAAGCACTAATCTTCACTCAGCGTGTCTGAGACGTTAGCGTGTGTTGGCAAG 638
Db 638 TGTTCAAGCTGCAAAATTTACATTTATCAGATTTTGAAGATGCTTCAAGTGTGACAAAG 697
Qy 639 GTGGGATTCGATGCTGCAACATCAATAGCCGTTTCAACGACCTTACTAGGCTGATTTGG 698
Db 698 GTGGGATTTGATGCCCGCACTAATCAATAGCTGTTAATATTAATTAATCACTAGGCTTATAG 757
Qy 699 AAATTAACCGACACGCGTGTGTTGTTGATCAACACTGCTTGAAGCGTGTGAGCGTGTGCGGTC 758
Db 758 CAATTAATACAGATATGCTGTAACCTGTGTCATACATACCGGATTAAGAGCTGTATGGGACC 817
Qy 759 TGATTTAGAGATTGATTAGATCAACCAAGTTGAGAGAGATTTGACCTCAGAGTTT 818
Db 818 GGATTTAGAGATTGATTAGATTAATCAATTTAGAAAGAAATTAACATCACTACGTAT 877
Qy 819 GGAATGTTGCTCTCTTCCCGAACTATGACTCCAGAACTTACCTTATCCGTACAGTGT 878
Db 878 AGATATGTTTCTCTATTTCCGAATATGATAGTAAAGATCAATTCAAACAGTTC 937
Qy 879 CCAACTTAACGAGAAATCTATTAACCCAGTCTTGAGAACTTCAGCGGTAGCTTCG 938
Db 938 CCAATTAACAGAAATTTATACAAACCCAGTATTAGAAATTTGATGATGTTTCG 997
Qy 939 TGGTTCTGCCAAGATTCGAAGGCTCCATCAGAGCCACACTTGATGACATCTTGAA 998
Db 998 AGGCTCGGCTCAGGCAATAGAGAGATTTAGAGTCCACATTTGATGATATACTTA 1057
Qy 999 CAGCATATCTATCTACACCATGCTCACAGAGAGATTTATAGTGTGACACCAAT 1058
Db 1058 CAGTATACCATCTATACGATGCTCATAGAGAGAAATTTATGTCATGAGGCACTCAAT 1117
Qy 1059 CATGAGCTCTCCAGTTGATTCAAGGCGCCGAGATTCTCTTCTCTCTATGAACTAT 1118
Db 1118 AATGGCTTCTCTGTAGGTTTTCGGGCGCAAGATTCATCTTTCGCTATATGAACTAT 1177
Qy 1178 GGGAAATCAGACTCCACAACACGATTTGTGCTCACTAGGTAGGCGGTGTATGAAAC 1237
Db 1238 AATATGCTCCCTTATATGAAGCCTTTTAAATATAGGATTAATTAATCAACATATC 1297
Qy 1239 CGTTCTTGAAGGAGATTCGCTATGAACTCTTCTTAATCTTGCATCGCTGTGTTA 1298
Db 1298 TGTTCTTGAAGGAGATTTGCTTATGAACTCTCTCAATTTGCAATCGGCTGATTA 1357

Db 361 CTTACTAATCCAGATTAAAGAAAGAGATGCGTATTCTCAATTCAATGATGAAACAGTCC 420
 Qy 517 TTGACCAAGCTATCCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTTCTCCGTG 576
 Db 421 CTTACAAACCGCTATTCCTTTTGGAGTTCAAAATTAATCAAGTTCCCTTTTATCAATA 480
 Qy 577 TACGTTCAAGCAAGCTAATCTTCACTCAGCGTCTTGAGACGTTAGCGTTTGGGCAA 636
 Db 481 TATGTTCAAGCTGCAAAATTTACATTTTCAAGTTTGGAGATGTTTCAAGTTTGGACAA 540
 Qy 637 AGGTTGGGATTCGATGCTGCAACATCATAGCGGTTTCAACGACCTTACTAGGCTGAT 696
 Db 541 AGGTTGGGATTTGATGCGGACATCAATAGTCTTAAATGATTTAACTAGGCTTAT 600
 Qy 697 GGAATCTACACGACCAAGCTGTTGTTGTATACAACACTGGCTTGGAGCGTGTGGGGT 756
 Db 601 GGCAACTATACAGATCAATGCTGTACGCTGTACAAATCGGGATTTAGACGCTGATGGGA 660
 Qy 757 CTTGATTTAGAGATTGGATTAGATACAAACGATTGAGAGAGAAATGACCTTCAAGTT 816
 Db 661 CCGGATTTAGAGATTGGATTAGATATCAATTTAGAGAGAAATTTAACTAACTGTA 720
 Qy 817 TTGGAATTTGCTCTCTTCCGAACTATGATCCGAACTCCATCCGTAAGCTG 876
 Db 721 TTGATATTCGTTCTCTATTTCGAACTATGATGATGAACTGATCCAACTTCAAGT 780
 Qy 877 TCCCACTTACAGAGAAATCTATATCAACCACTTCTTGAACCTTGCAGCTAGCTTC 936
 Db 781 TCCCAATTTACAGAGAAATTTATACAAACCACTATTTAGAAATTTTGAATGATGTTT 840
 Qy 937 CGTGTCTTCCCAAGGATTTGAAGGCTCCATCAGAGCCCACTTGTAGCATCTTG 996
 Db 841 CGAGGCTCGGCTCAGGGCATGAAGAGATTTAGAGTCCCACTTTGATGAAATACTT 900
 Qy 997 AACGCAATTAATCTATACAGGATGCTCAGAGAGAGATTTCTGCTGAGACACCAG 1056
 Db 901 AACGATTAATCAATCTATACGATGCTCAGAGAGATTTATGCTCAGGGCATTA 960
 Qy 1057 ATCATGCTCTCCAGTTGATGATGAGCGGCGCGGATTTACCTTCTCTATGAACT 1116
 Db 961 ATATGCTTCTCCGTAAGGTTTTCGGGCGCAAGATTTCACTTTCCGCTATAGGAACT 1020
 Qy 1117 ATGGAAACCGCGCTCCCAACAAAGTATCGTTGCTCACTAGAGTCAAGGTTCTACGA 1176
 Db 1021 ATGGAAATGACGCTCCCAACAAAGTATGCTGCTCACTAGGTCAGGGCGTGTATGA 1080
 Qy 1177 ACCTGCTTCCACTTGTACAGAAAGACCTTCAATACGCTATCAAAACCAAGAACTT 1236
 Db 1081 ACATTAATGCTCACTTATATAGAAAGACCTTTAATATAGGATTAATATCAACACTTA 1140
 Qy 1237 TCCGTTCTTGAAGAAAGAGTTCGCTATGAAACCTTCTTAACTTCCATCCGCTGT 1296
 Db 1141 TCTGTTCTTGAAGGAGAAATTTGCTATGAAACCTCTCAAAATTTCCATCCGCTGTA 1200
 Qy 1297 TACGAAAGAGCGGAACCGTTGATCTTGGACGAATCCACACAGAAACAATGTG 1356
 Db 1201 TACGAAAGAGCGGAACCGTATGATCTGATGAAATACCGCCACAGAAATCAACCTG 1260
 Qy 1357 CCACCCAGGAGAGATTTCCCAACAGTTGAGCCAGCTGTCATGTTCCGTTCCGAGTTC 1416
 Db 1261 CCACCTAGGAGAGATTTAGTATGATTTAGCCAGTTTCAATGTTTCCGTTCCGAGTTC 1320
 Qy 1417 AGCAACAGTTCCGTAGAGCATCAGAGCTCTATGTTCTGATGATTCATCTGATGCT 1476
 Db 1321 AGTATATAGTAGTATATATATAGAGCTCTATGTTCTTGGATATCATCTGATGCT 1380
 Qy 1477 GAGTTCAACATATATCTCTCTCTCAATCAACCAATCCCTTGAACCAAGTACT 1536
 Db 1381 GAAATTAATATATATATCTTCAATCAACAAATTAACCAAAATCTTAAACAAATCTACT 1440
 Qy 1537 AACCTTGATCTGAACCTTCTGCTGAAAGAGACGAGCTTACAGAGAGTATTTCTT 1596
 Db 1441 AATCTTGCTCTGAACTTCTGCTGTTAAAGAACAGATTTTACAGAGAGATATTTCTT 1500

Qy 1597 AGAAGACTTCTCTGCGCCAGATTAGCAACCTCAGAGTTAATCACTGACCACTTCT 1656
 Db 1501 CGAAGACTTCACTGCGCCAGATTATCAACCTTAAAGATTAATATACCTGACCACTTATCA 1560
 Qy 1657 CAAAGATATGCTGCAGAGATTGCTTACGAAATCAACCTTAACTTGAATTCACACCTCC 1716
 Db 1561 CAAAGATATGCTGCAGAAATTCGCTACGCTTCAACCAATTTACAAATTCATATCAATCA 1620
 Qy 1717 ATCGACGAAGGCTTCAATCAAGGATTAATCTTCCGCAACCATGTCAAGCGGAGCAAC 1776
 Db 1621 ATTACGGAAGACCTTAAATTAATCAAGGAAATTTTACACAACTATGATGAGGAGATAT 1680
 Qy 1777 TTGCAATTCGCGACCTTCAAGACCGTCTTCACTAATCTTCAATCTTCAACGGA 1836
 Db 1681 TTACAGTCCGGAAGCTTTAGAGATGATGATTTTACTACTCCGTTTAACTTTCAAAATGGA 1740
 Qy 1837 TCAAGCTTTTCAACCTTACGCTCAATGTTGTTCAATCTGCAATGAAATGATTAATGAC 1896
 Db 1741 TCAAGTATTTTCAAGTATGCTCATGCTTCAATTCAGGCAATGAAATTTATATGAT 1800
 Qy 1897 CGATTGATTTTGTGCTGCGGAGATTACCTTCAAGCTGAGTA 1940
 Db 1801 CGAATTGAATTTGTTCCGCGAGAAATTAACCTTTGAGGAGATATA 1844

 RESULT 11
 US-10-035-060-7
 : Sequence 7, Application US/10035060
 : Publication No. US20030040619A1
 : GENERAL INFORMATION:
 : APPLICANT: Edwards, David
 : APPLICANT: Wong, Siu-Yin
 : APPLICANT: Herrnstadt, Corinna
 : APPLICANT: Milcox, Edward
 : TITLE OF INVENTION: Process For Altering the Host Range Or Increasing The
 : TITLE OF INVENTION: Toxicity Of
 : TITLE OF INVENTION: Bacillus Thuringiensis Lepidoteran Toxins, and Recombinant DNA
 : FILE REFERENCE: M12C1FDF3D1
 : CURRENT APPLICATION NUMBER: US/10/035, 060
 : PRIOR FILING DATE: 2001-12-27
 : PRIOR APPLICATION NUMBER: 09/405, 788
 : PRIOR FILING DATE: 1999-09-27
 : PRIOR APPLICATION NUMBER: US 08/580, 781
 : PRIOR FILING DATE: 1995-12-29
 : PRIOR APPLICATION NUMBER: US 08/420, 615
 : PRIOR FILING DATE: 1995-04-10
 : PRIOR APPLICATION NUMBER: US 08/097, 808
 : PRIOR FILING DATE: 1993-07-27
 : PRIOR APPLICATION NUMBER: US 07/980, 128
 : PRIOR FILING DATE: 1992-11-23
 : PRIOR APPLICATION NUMBER: US 07/803, 920
 : PRIOR FILING DATE: 1991-12-06
 : PRIOR APPLICATION NUMBER: US 07/356, 599
 : PRIOR FILING DATE: 1989-05-24
 : PRIOR APPLICATION NUMBER: US 06/904, 572
 : PRIOR FILING DATE: 1986-09-05
 : PRIOR APPLICATION NUMBER: US 06/808, 129
 : PRIOR FILING DATE: 1985-12-12
 : NUMBER OF SEQ ID NOS: 9
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 7
 : LENGTH: 3531
 : TYPE: DNA
 : ORGANISM: Bacillus Thuringiensis
 US-10-035-060-7

 Query Match 43.0%, Score 1197.6, DB 14, Length 3531,
 Best Local Similarity 78.1%, Pred. No. 0,
 Matches 1440, Conservative 0, Mismatches 404, Indels 0, Gaps 0,
 Qy 97 ATGAGACAACCAACCAATCAAGAAATGCAATTCATATCACTGCTGTAACCCAGAA 156

Db 1 ATGATATACATCCGATCATATGAATGATCTCTATATTTGTAAGTAACTCGAA 60
Qy 157 GTTGAAGTACTTGGGAGAAAGCATTTGAACCGGTTACATCTCCATCGATCCCTG 216
Db 61 GTAGAAGTATTAGGGAGAAAGATAGAACTGGTTACACCCCAATGATATTTCTTG 120
Qy 217 TCCTTGAACACAGTTTGTGCTCAGGAGATTCGTGCAGAGTGTGGTTGTTCTCGA 276
Db 121 TCCGTACGCAATTTCTTTAGTGAATTTGTTCCCGGTGCTGATTTGTGTAGACTA 180
Qy 277 GTTGAATCATCTGGGGATCTTTGTGTCATCTCAATGGATTCATTTCTGTGCAAT 336
Db 181 GTTATATATATGGGGAATTTTGGTCCCTCTCAATGGAGCGCATTTCTGTCAAA 240
Qy 337 GAGAGTGTATCAACCAAGATCGAAGATTCGCGAGAAACGAGCATCTAGAGTGG 396
Db 241 GAACGTTAATTAACCAAGAAATAGAAATTCGTAGAAACCAAGCCATTTCTAGAT 300
Qy 397 GAAGGATGAGCAATCTCTACCAATCTATGCAAGAGCTTCAGAGAGTGGAAAGCC 456
Db 301 GAAGGATGAGCAATCTTATCAATTTAGAGAAATCTTTAGAGAGTGGAAAGCA 360
Qy 457 CTTACTAATCCAGCTCTCCGAGAGAAATGCGTATTCATTCACAGATGAACGCC 516
Db 361 CTTACTAATCCAGCTTAAAGAGAGATGCGTATTCATTCATGATGAACAGTCC 420
Qy 517 TTGACCAAGCTATCCATGTTGGCAGTCCAGAACTCAAGTCCCTCTGTGCGTG 576
Db 421 CTTACACCGCTATCTCTTTTGCAAGTCAAAATTAACAAATTCCTTTTATCAG 480
Qy 577 TACGTTCAAGAGCTAATCTTCACTCAGCGTCTTCGAGAGCTTAGCGTTTGGG 636
Db 481 TATGTTCAAGCTGCAATTTATCATTTATCAGTTTGAAGAGATTTTCAAGT 540
Qy 637 AGTGGGATTCGATGCTGCAACATCAATAGCCGTTCAACAGACTTATAGGCT 696
Db 541 AGTGGGATTTGATGCGCGCATATCAATAGTCTTAAATGATTAATCAGGCT 600
Qy 697 GGAATCTACCGGACCGAGCTGTTGGTGTACCACTGCGTGGAGGCTCGGG 756
Db 601 GGAATCTACCGAGATTTAGCTGTACGCTGTACAAATGCGGATTAAGAGT 660
Qy 757 CTTGATCTAGAGATTTGATAGATTAACAACAGTTCAAGAGAAATGACCTCA 816
Db 661 CCGGATTTAGAGATTTGGGTAGATATCAATTTAGAGAGAAATTAACAT 720
Qy 817 TTGACATTTGTCTCTCTCCGAACTATGACTCCAGAACTTACCTATCCGT 876
Db 721 TTAGATATCGTGTCTCTCTCCGAAATTAATGATAGTAGAATTCCAATTC 780
Qy 877 TCCCACTTACCGAGAAATCTATCTAACCCAGTTCTTGAACCTTGAAGCT 936
Db 781 TCCCACTTACCGAGAAATTTATACAAACCCAGATTAAGAAATTTGATG 840
Qy 937 CGTGTCTTCCCAAGATATCGAAGCTTCATCAGAGCCCACTTGAATGCA 996
Db 841 CGAGCTCGGCTCAGGGCATAGAGAGATTTAGAGAGTCCACATTTGATG 900
Qy 997 AACAGATATCTATCTACACCGATGTCTACAGAGAGATTTACTGTCTGAC 1056
Db 901 AACAGATATACCATCTATACGATGTCTCTAAAGGGAAATATATGTCAG 960
Qy 1057 ATCATGAGCTCTTCCAGTTGATTCAGCGGGCCGAGTTTACCTTCTCTAT 1116
Db 961 ATTAATGCTTCTCTGTAGGGTTTTCGGGCCAGAAATTAATTTCCGTAT 1020
Qy 1117 ATGGGAAAGCGGCTTCACAAACGATCTGTTCTCAACTAGTCAAGGCTCT 1176
Db 1021 ATGGGAAATGCAAGCTCCACAAACGATTTGTTGCTCACTAGTCAAGGCT 1080
Qy 1177 ACCTGTCTTCAACCTTGTACGAAGACCTTCAATATGATCAACACGAACT 1236

Db 1081 ACATTAATCTTCACTTATATAGAACTTTAATATAGAGTAAATATCAACACTA 1140
Qy 1237 TCGGTTCTTGAACGGAACAGAGTTTCGCTTATAGAACTCTTCTAATCTTCCATCGCTGT 1296
Db 1141 TCTGTTCTTGAACGGAACAGAGTTTTCGTTATAGAACTCTTCAATTTGCCATCGCTGT 1200
Qy 1297 TACAGAAAGCGGAACCGTTGATTCCTTGTAGAGAAATCCACCAAGAAACATATGT 1356
Db 1201 TACAGAAAGCGGAACCGTATGATTCGCTGATGAAATACCGCACAGAAATACACGTG 1260
Qy 1357 CCACCCAGGAAGATTCCTCCACAGGTATAGCCAGCTGCATGTCGTTCCGTTCCGATTC 1416
Db 1261 CCACCTAGGCAAGATTTAGTCATGATTAAGCCATGTTCAATGTTTCGTTCAAGCTTT 1320
Qy 1417 AGCAACAGTTCCGAGCATCATAGAGCTCTTATGTTCTCATAGATTCATGATGCT 1476
Db 1321 AGTAATAGTATGTAATATATATAGAGCTCCAAAGTTTCTTGGCAGCATCCGAGTCT 1380
Qy 1477 GAGTTCAACATATCATCTCTCTCTCTCAATCAACCAATCCATGACCAAGTCTAT 1536
Db 1381 GAATTTAATATATATATCTCTTCAATCAAAATTAACAAATACCTTTAACAAATCTACT 1440
Qy 1537 AACCTGATCTGGAATCTGTGTGAAAGGACAGAGCTTCACAGAGGTGATTTCTT 1596
Db 1441 AATCTGCTGTGAACTTCTGTCTGTAAAGACAGAGATTTACAGAGAGATATTTCTT 1500
Qy 1597 AGAAGACTTCTCTGCGCAGATTAAGCACTCCAGATTAACATCACTGACCACTTCT 1656
Db 1501 CGAAGACTTCACTGCGCAGATTTCAACCTTAAGATTAATATATGACCACTTATCA 1560
Qy 1657 CAAGATATCTGTGAGATTCGTTAGCATCTACCACTTCACTTCACTGACCACTCTC 1716
Db 1561 CAAGATATCTGAGATTCGTTAGCATCTACCACTTCACTTCACTTCACTGACCACT 1620
Qy 1717 ATCGAGGAGGCTTATCAATCAGGATTAATCTCCGCAACCATGTCAGGAGGAGCAAC 1776
Db 1621 ATTAACGGAACCTTATTAACAGGATTAATTTTCAAGCACTTATGAGTGGAGAT 1680
Qy 1777 TTGCATCTCGGACCTTCAGAACCGTGGTTTCACTACTCTTCAACTTCTTCAACGGA 1836
Db 1681 TTACAGTCCGGAACCTTGAAGCTGATGATTTACTCTGTTTCACTTCAATGGA 1740
Qy 1837 TCAGGCTTTCACCTTGAAGCTGATGTTCAATTTGCAATGAAATGATGATGAC 1896
Db 1741 TCAAGTATTTAGGTTAAGTGTCTCATCTTCAATTCAGGCAATGAAGTTTATATGAT 1800
Qy 1897 CGTATGAGTTTGTGCTGCGGAGATTAACCTTGAAGGCTGAT 1940
Db 1801 CGAATGATTTGTTCCGCGAGAGTACCTTTGAGCGAGATA 1844

RESULT 12
US-10-035-060-3
Sequence 3, Application US/10035060
Publication No. US20030040619A1
GENERAL INFORMATION:
APPLICANT: Edwards, David
APPLICANT: Wong, Siu-Yin
APPLICANT: Herrnsfeldt, Corinna
APPLICANT: Wilcox, Edward
TITLE OF INVENTION: Process For Altering the Host Range Or Increasing The
TITLE OF INVENTION: Toxicity Of
TITLE OF INVENTION: Bacillus Thuringiensis Lepidopteran Toxins, and Recombinant DNA
FILE REFERENCE: M12C1FDF3D1
CURRENT APPLICATION NUMBER: US/10/035, 060
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 09/405, 788
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 08/580, 781
PRIOR FILING DATE: 1995-12-29
PRIOR APPLICATION NUMBER: US 08/420, 615
PRIOR FILING DATE: 1995-04-10

PRIOR APPLICATION NUMBER: US 08/097,808
 PRIOR FILING DATE: 1993-07-27
 PRIOR APPLICATION NUMBER: US 07/980,128
 PRIOR FILING DATE: 1992-11-23
 PRIOR APPLICATION NUMBER: US 07/803,920
 PRIOR FILING DATE: 1991-12-06
 PRIOR APPLICATION NUMBER: US 07/356,599
 PRIOR FILING DATE: 1989-05-24
 PRIOR APPLICATION NUMBER: US 06/904,572
 PRIOR FILING DATE: 1986-09-05
 PRIOR APPLICATION NUMBER: US 06/808,129
 PRIOR FILING DATE: 1985-12-12
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3
 LENGTH: 3531
 TYPE: DNA
 ORGANISM: Bacillus thuringiensis
 US-10-035-060-3

Query Match 42.8%; Score 1194.4; DB 14; Length 3531;
 Best Local Similarity 78.0%; Pred. No. 0;
 Matches 1438; Conservative 0; Mismatches 406; Indels 0; Gaps 0;

97 ATGACAAACAAACCAACATCAAGATGATCCATCACTGCTTGAGTAAACCCAGAA 156
 1 ATGAGATAACATCCGACATCAATGATGATCTCTATATGTTTAACTGAA 60
 157 GTTAAGACTTGTGGAGAGCATGTAACCGGTTCACTCCCATGATCTCCCTG 216
 61 GTAGAAGATTAGGGGAGAAAGATAGAACTGGTTACACCCCAATGATATATCTTG 120
 217 TCCTTGACACAGTTTCTGCTCAGCAGATCGTGCCAGGTGCTGGTTCTGCGACTA 276
 121 TCGCTAACGCAATTTCTTTAGTGAATTTGTTCCGGTGTGATTTGTTAGACTA 180
 277 GTTGACATCATCTGGGGTATCTTTGGTCAATCTCAATGGATTCGATTCCTGGTCAATT 336
 181 GTTGATATATATGGGAAATTTTGGTCCCTCAATGGAGCGCATTTCTGTCAAAATT 240
 337 GAGCAGTGATCAACCAAGAGATGAGATTCGCGCAGAAACGAGCCATCTAGGTG 396
 241 GAACGTTAATTAACCAAGATAGAAATTCGTTAGAACCAACCAATTTCTAGATTA 300
 397 GAAGATTAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGATGGGAAGCCGAT 456
 301 GAAGACTAAGCAATCTTTATCAATTTACGAGAACTTTTAGAGATGGGAAGCAGAT 360
 457 CCTACTAACCAAGCTCTCCGAGAGAAATGCGTATTTCAATTCAGACATGACAGCC 516
 361 CCTACTAATCCAGCAATTAAGAGAGATGCGTATTTCAATTCAGACATGACAGTCC 420
 517 TTGACCAAGCTTCCAGTGTGGCAGTCCGAACTCAAGTTCCTCTGTGCGGTG 576
 421 CTTAACCGGATTTCTCTTTTGGAGTTCAAAATTTCAAGTTCCTCTTTTATCAGTA 480
 577 TACGTTCAAGCAGTATCTTCACTCAGCGTCTTGAGACGTTAGCGTGTGGGCA 636
 481 TATGTTAAGCTGCAATTTTACATTTATCAGTTTGAAGAGATTTTCAAGTGTGGACA 540
 637 AGGTGGGATTCAGTGTGCAACATCAATAGCCGTTACAGACCTTACTAGGCTGATT 696
 541 AGGTGGGATTTGAGCGCGCACTATCAATAGTCTTATATGATTTTAACTAGGCTTATT 600
 697 GGAATCAACCGACAGCGTGTGGTGTACCAACATGCTTGAGAGGTGCTGGGAT 756
 601 GGCAACTATACGATTAAGCTTACGCTGTACAAATTCGCGATTAGAACGTATAGGGA 660
 757 CCTGATTCAGAGATTGATTAAGATACCAAGTTCAAGAGAAATTGACCCCTCAAGTT 816
 661 CCGGATTCAGAGATTGGGTAGGATATATCAATTTAGAAAGAAATTAACACTAAGTGA 720
 817 TTGGACATTTGTCTCTCTTCCGGAATATGACTCCAGAACTTACCTATCCGTACAGTG 876

721 TTGATATCGTCTCTGTTCCGAATTATGATAGATGATCAATTTCAACGTT 780
 877 TCCCAACTTACAGAGAAATCTATTAACCCAGTTCTTGAGAACTTGAAGGTTCTC 936
 781 TCCCAATTAACAGAGAAATTTATCAAAACCGATTTAGAAATTTTGAATGATTTT 840
 937 CGTGTTCCTCCCAAGGATTCGAAGGCTCATCAGAGCCCACTTGAATGACATTTTG 996
 841 CGAGGCTCGGCTCAGGCGATAGAAAGATTAAGAGTGCACATTTGATGATATATCTT 900
 997 AACAGCATTAATCTTACACCGATGCTCAGAGAGAGATTAAGTGTGAGACACAG 1056
 901 AACGATTAATCAATCTATACGATGCTCAGAGAGGTTATTAATTTGATGAGGATCA 960
 1057 ATCATGCTCTCTCAGTTGATTCAGCGGCGCCAGTTTACCTTCTCTATGAACT 1116
 961 ATATGCTCTCTCTGATAGGTTTTGGGGCCGAATTTCACTTTCCGCTATATGAACT 1020
 1117 ATGGAAACGCCGCTCCACAACAAGTATGTTGCTCACTAGTCAAGGTTCTACAGA 1176
 1021 ATGGAAATCAGCTCCACAACAAGTATGTTGCTCACTAGTCAAGGCTGATATAGA 1080
 1177 ACCTGTCTTCCACTTGTACAGAGACCTTCAATGCTGTTACAAACCAACCACTT 1236
 1081 ACATTTATGCTCACTTATATAGAGACCTTTATATAGGATTAATTAATCAACACTA 1140
 1237 TCGTCTTACAGGAACAGATTCGCTATGAACTCTTCTAATCTTCCATCCGCTGT 1296
 1141 TCTGTTCTTACAGGAGAGAAATTTGTTATGAAACCTCTCAAAATTTGCCATCCGCTGA 1200
 1297 TACGAAAGACCGAACCGTTGATTCCTTGAAGAAATCCACCAACAACAAATGTG 1356
 1201 TACAGAAAGACCGAAGGTAGATTCGCTGATGAAATACCGCAAGAAATACAAAGTG 1260
 1357 CCACCCAGGAGGATTTCTCCACAGGTGAGCAGCTGTCATGTTCCGTTCCGATTC 1416
 1261 CCACCTGGCAAGGATTTAGTCAATGATTAAGCATGTTTCAATGTTTCTGTTACGCTTT 1320
 1417 AGCAACAGTTCCGTGACATCATCAGAGCTCTATGTTCTCATAGATTCATCTGATGCT 1476
 1321 AGTAATGATGATTAATTAATTAAGAGCTTCAACGTTTCTTGGCAGCATCCGATGCT 1380
 1477 GAGTTCAACATTAATCTTCTCTCTCTCAAAATCAACCAATCCATGAGCAAGTCTACT 1536
 1381 GAATTTAATTAATTAATTTCTTCAATCAAAATTAACAAATTAACCTTTAAACAAATCTACT 1440
 1537 AACCTGATCTGGAATCTTCTGTGTGAAAGAGCAGGCTTCAAGAGGATGATTTCTT 1596
 1441 AATCTTGGCTGTGAATCTTCTGTGTGAAAGAGCAGGATTTTACAGAGAGATATTTCTT 1500
 1597 AGAAGAACTTCTCTGCGCAGATTAGCACTCAGATTAATCACTGACCACTTCT 1656
 1501 CGAAGAACTTCACTGGCAGATTTCACCTTAAGAGAAATFATTAATGACCACTATCA 1560
 1657 CAAGATATGCTGAGGATTCGTTACGATCTACCACTAATCTTGAATTCACACCTCC 1716
 1561 CAAGATATCGGTAAGAAATTCGCTACGCTTCTCACTCAAAATTAACATTCATCAATCA 1620
 1717 ATGACGGAAGGCTTATCAATCAGGATTAATCTTCCGCAACCATGTCAAGGCGAGCAAC 1776
 1621 ATTAACGGAACCTATTAATCAAGGATTAATTTTTCAGCACTATGATAGTGGAGATTAAT 1680
 1777 TTGCAATCCGACAGCTTACAGAACCGTGGTTTCACTCTCTTCAATCTTCTCAACGA 1836
 1681 TTACAGTCCGAACTTTAGAGCTGTAGGTTTACTACTCGTTTAACTTTTCAAAATGGA 1740
 1837 TCAAGCGTTTCAACCTTAAAGGCTCATGTTGTTCAATTTGCGCAATGAAGTATAC 1896
 1741 TCAAGTATTTTAAAGTAAAGGCTCATGTTTCAATTTCAAGCAATGAAGTTTATATGAT 1800
 1897 CGTATGAGTTGTGCTGCGCAAGTTAATCTTCAAGGCTGAGTA 1940

Db 1441 AATCTGCTCTGAACTTCTGTCTTAAAGACAGAGATTATACAGAGAGATATCTT 1500
Qy 1597 AGAAGACTTCTCTGCGCAGATTAAGACCTCAGAGTTAATCATCTGACCACTTCT 1656
Db 1501 CGAAGAACTTACCTGGCCAGATTTCAACCTTAAAGATTAATTTACTGCACTTATCA 1560
Qy 1657 CAAAGATATCGTGTCAAGATTCTTTAGCATCTACCACTTAATTGCAATTCACACTCC 1716
Db 1661 CAAAGATATCGGTAAAGATTCGCTACGCTTCTACTCAAAATTTACATTCATATCA 1620
Qy 1717 ATGACGGAAGCCTTATCATCAGGTTACTTCCGCAACATGTCAAGCGGACAC 1776
Db 1621 ATTACCGGAAGACCTATTAATCAGGTTAATTTTTCAGCACTATGAGTAGGAGTAAT 1680
Qy 1777 TTGCAATCCGCGACGTTCAAGACGTCGGTTTCACTACTCTTCAACTTCTTAAGGA 1836
Db 1681 TTACAGTCCGGAAGCTTTAGAGCTGTAGGTTTACTACTCCGTTTAACTTTCAAAATGA 1740
Qy 1837 TCAAGCGTTTTCACCCCTTAGCGCTCATGTCTTCAATTCGTGCAATGAAGTACATTGAC 1896
Db 1741 TCAGGTGATTTACGTTAAGTCAATGCTCATGTCTTCAATTCAGGCAATGAAGTTATATGAT 1800
Qy 1897 CGTATGAGTTTGTGCTGCGCGAAGTTACCTTCGAGCGTGA 1940
Db 1801 CGAATGAAATTTGTTCGCGCAGAGTAACCTTTGAGCGCAATA 1844

RESULT 14

US-10-102-469-1
; Sequence 1, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: synthetic structural gene encoding B.t.k. HD-1 insecticidal prote
; OTHER INFORMATION: in
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1743)
; OTHER INFORMATION:
US-10-102-469-1

Query Match 42.4%; Score 1180.8; DB 12; Length 1743;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 189; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

Qy 181 ATTGAACCGGTAACTCCATGCACATCTCTGCTTGAACACAGTTTCTGCTACG 240
Db 7 ATAGAACAATGTTAAACCCCAATGATATTTCTTGTGCTAAACCAATTTCTTTGAGT 66
Qy 241 GAGTTCGTGCGAGTGTGCTGCTTCCGACTAGTTGACATCATCTGGGGTATCTTT 300
Db 67 GAATTTGTTCCCGGTGCTGATTTGTGTTAGACTAGTTGATTAATTCGCGGAATTTT 126

Qy 301 GGTTCATCTCATGAGATGATCTCTGTGCAAAATTGACAGTTGATCAACAGAGATC 360
Db 127 GGTTCCTCTCAATGGGACGATTTCTGTCAAAATTGAACAGCTCATCAACAGAGATC 186
Qy 361 GAAGATTTGCCAGGAACCGAGCATCTCTAGSTTGGAGAGATTTGACATCTCTACCA 420
Db 187 GAAGATTTGCTAGGAATCAAGCATTTCTAGATTAAGAAAGACTTAAGCAATCTTATCA 246
Qy 421 ATCTATGACAGAGCTTCAAGAGTGGAGAGCCGATCTCTAATCCAGCTCTCCGAG 480
Db 247 ATTTAGCAGAAATCTTTTGAAGAGTGGAGAGAGATCTCTAATCCAGATTAAGGA 306
Qy 481 GAAATGCTATTAATTAATCAACGATGAACAGCGCTTGAACAAGCTATTCATGTTTC 540
Db 307 GAGATGGTATTAATTAATCAATGACATGAACAGTGCCTTCAACCGCTATTCCTTTT 366
Qy 541 GCAATCCAGAACTTCAACGATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 367 GCAATTCAAATTAATCAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 426
Qy 601 CTCAGCGCTGCTGAGAGCTTACGCTGTTTGGCAAAAGTGGGATTCGATGTCGAAC 660
Db 427 CTCCTAGTTTGAAGATGTTTCAATGTTTGAACAAAGTGGGATTTGATGCGGACT 486
Qy 661 ATCAATGCGCTTCAACGACCTTACTAGCTGATGGAATCAACGACGACGCTGTT 720
Db 487 ATCAATGCTGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 546
Qy 721 CGTTGTTCAACACTGCTTGAAGCGTCTGAGCGTCTGAGGCTCTGATTTAGAGATTGA 780
Db 547 CGCTGTACAAATGCGGATTAAGCGTGTATGGGACCGGATTTCAAGATTTGATACG 606
Qy 781 TACAACAGTTTCAAGAGATTTGACCCCTCAAGTTTGGACATTTGTCTCTCTCCG 840
Db 607 TACAACAGTTTCAAGAGATTTGACCCCTCAAGTTTGGACATTTGTCTCTCTCTCCG 666
Qy 841 AACTATGATCCAGAACCTTACCTTATGCTGTAAGTGTCCCACTTACCAAGAAATCTAT 900
Db 667 AACTATGATGTAAGAAAGTATCCAAATTCGAACAGTTTCCAAATTAACAGAAATTTAT 726
Qy 901 ACTAACCAGTTCTTGAACCTTCAAGGTAAGTCTCGTGTCTGCTGCTGCTGCTGCTG 960
Db 727 ACAAAACCAATTAAGAAATTTGATGATGTTTGAAGCTGCTGCTGCTGCTGCTGCTG 786
Qy 961 GGCTCATTCAGAGCCCACTTGTATGAGATCTTGAACAGATTAATCTATCTACACGAT 1020
Db 787 GGAAGTATTAAGAGTCCACATTTGATGATATCTTAATGATTAACATCTATACGAT 846
Qy 1021 GCTCAAGAGAGATTAATCTGCTGTAACACCAATCATGCTCTCTCAAGTTGATTC 1080
Db 847 GCTCATAGAGAGATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
Qy 1081 AGCGGCGCGAGTTTACTCTTCTCTATGGAATTAAGGAATTAAGGAATTAAGGAATTA 1140
Db 907 TCGGCGCGAGATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966
Qy 1141 CGTATGCTGCTCAATAGTCAAGTGTCTTACAGAACTTGTCTTCACTTCACTTACAGA 1200
Db 967 CGTATGCTGCTCAATAGTCAAGTGTCTTACAGAACTTGTCTTCACTTCACTTACAGA 1026
Qy 1201 AGACCTTCAATATGCGTATTAACCAACAGAACTTCTGCTTGAACAGAGATTC 1260
Db 1027 AGACCTTCAATATGCGGATTCMAAACCAATATCTGTTTGAACAGAGATTC 1086
Qy 1261 GCTATGGAACCTTCTTCAATCTGCTGCTGCTGCTTGAACAGAGAGAGAGAGAGAGAT 1320
Db 1087 GCTATGGAACCTTCTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146
Qy 1321 TCCTTGAAGAAATCCACCAAGAAACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1147 TCGCTGATGAATTAACGCGCAGAAATTAACAACTGCTGCTGCTGCTGCTGCTGCTGCT 1206

QY	138	AGGTTGAGCCAGTGTCATGTCGCGTCCGGATTCAGCAACAGTTCGGTAGCATATC	1440
Db	1207	CGATTAAAGCCATGTTTCATGATGTTTCGTTACAGCTTTAGTAATAGTAGCTAAGTAATA	1266
QY	1441	AGAGCTCCCTAATGTTCTCATGGAATTCATGTAGTGCGAGTTCAACAAATATCATTTCTTCC	1500
Db	1267	AGAGCTCCTTAATGTTCTCTTGGATATCATGTGTGCGTAGTTCAACAAATATCATTTCTTCA	1326
QY	1501	TCTCAAAATACCCAAATGCCAATTCAGTCAAGTCTACTAATCTTGATCTCGAAGCTTCGTG	1566
Db	1327	TCACAATACCCAAATGCCAATTCAGTCAAGTCTACTAATCTTGATCTCGAAGCTTCGTG	1386
QY	1561	GTGAAGGACAGAGCTTCACAGAGGTATATTTCTTAGAAGACTTCTCTGGCCAGATT	1620
Db	1387	GTTAAAGGACAGAGATTTCACAGAGGATATTTCTTCGAAGAACTTCACCTGGCCAGATT	1446
QY	1621	AGCAACCCCAAGTTAATCATCATCTGCACACATTTCTCAAAATATCGTGTCAGATTGCT	1680
Db	1447	TCAACCTTAAAGTAATATTAATTCACACATTTATACAAAGATATCGGGTAAGAAATTGCG	1506
QY	1681	TACGCATCTACCACTAATCTTSCAATTCACACCTTCATCGAAGGAGGCTATCAATCAG	1740
Db	1507	TACGCTTACCAACAAACCTTCAGTTCCACACATCAATTCAGGAAAGACCTATTATACAG	1566
QY	1741	GCTAATCTTCTCCGCAACCATGTCAAGGGGACAGCACTTGCAATCCGGACGTTTCAGAAC	1800
Db	1567	GGGAATTTTTAGCAACATATAGTAGTAGGAGTAATTTACAGTCCGGAAGCTTTAAGAACT	1626
QY	1801	GTCGGTTTCACTACTCTTTCAACTCTCTAAGCATCAAGCGTTTCAACCTTAAGCCCT	1860
Db	1627	GTAAGTTTACTACTCCGTTTAACCTTTCAATGATCAAGTAGTATTACGTTAATAGTCT	1686
QY	1861	CATGTGTTCAATTTCTGCGCAATGAAGTGAATTAACCGTATTTAGAGTTGTGCTTC	1916
Db	1687	CATGCTTTCATTCAGGCAATGAAGATTATATAGTATGAATTTGTTGCTCCGC	1742

RESULT 15

1 Sequence, Application US/09988462
2 Publication NO. US20030046726A1
3 GENERAL INFORMATION:
4 APPLICANT: Kozieł, Michael G.
5 Desai, Nalini M.
6 Lewis, Kelly S.
7 Kramer, Vance C.
8 Warren, Gregory W.
9 Evola, Stephen V.
10 Crossland, Lyle D.
11 Wright, Martha S.
12 Merlin, Ellis J.
13 Lannis, Karen L.
14
15 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
16 INSECTICIDAL ACTIVITY IN MAIZE
17
18 NUMBER OF SEQUENCES: 94
19 CORRESPONDENCE ADDRESS:
20 ADDRESSEE: Syngenta Biotechnology, Inc.
21 STREET: 3054 Cornwallis Road
22 CITY: Research Triangle Park
23 STATE: NC
24
25 COUNTRY: USA
26
27 ZIP: 27709
28
29 COMPUTER READABLE FORM:
30 MEDIUM TYPE: Floppy disk
31 COMPUTER: IBM PC compatible
32 OPERATING SYSTEM: PC-DOS/MS-DOS
33 SOFTWARE: Patent In Release #1.0, Version #1.30
34
35 CURRENT APPLICATION DATA:
36 APPLICATION NUMBER: US/09/988,462
37 FILING DATE: 20-NO. US20030046726A1-2001
38
39 CLASSIFICATION: <Unknown>
40
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: US 09/547,422

Query Match	Best Local Similarity	Matches 1413	Conservative	0	Mismatches 432	Indels	0	Gaps	0
Query 97	ATGCACCAACACCCAAATCAAGCAATGCATTCATACAACTGTTAGTAAACCCAGAA	156							
Db 1	ATGCACCAACACCCAAATCAAGCAATGCATTCATACAACTGTTAGTAAACCCAGAA	60							
Query 157	GTTGAAGTACTGTTGGTGAAGAACGCAATGAACCCGGTTACACTCCCATGCACATCTCTCTG	216							
Db 61	GTGAGAGTCTGGGGGGGAGGAGCGATCGAAGCCGGCTACACCCCATGCACATCAGCCCTG	120							
Query 217	TCCTTGAACAAGTTTCTCTCAAGCAGATTCTGTCAGAGTCTCTGGTTCTTCGACATC	276							
Db 121	AGCCGAGCCAGTTCTCTCTGAGCAGATTCTGTCAGAGTCTCTGGTTCTTCGACATC	180							
Query 277	GTTGACATCATCTGGGGATATCTTTGTCATCTCAATGAGGATGCATTCCTGTGCAATT	336							
Db 181	GTGACATCATCTGGGGATATCTTTGTCATCTCAATGAGGATGCATTCCTGTGCAATT	240							
Query 337	GAGCAGTGTATCAACACAGAGATCGAAGATTGCGCAGAGAACCGACCATCTCTAGGTTG	396							
Db 241	GAGCAGTGTATCAACACAGAGATCGAAGATTGCGCAGAGAACCGACCATCTCTAGGTTG	300							
Query 397	GAAAGATTGAGCAATCTTACCAATCTATGAGAGAGCTTCAGAGAGTGGGAGCGCAT	456							
Db 301	GAGGAGCTGAGCAATCTTACCAATCTATGAGAGAGCTTCAGAGAGTGGGAGCGCAT	360							
Query 457	CCTACTTAACCCAGCTCTCCGCGAGGAAATGCGTATTTCAATTCAACGACATGAAACAGCGC	516							
Db 361	CCACCAACCCCGCTCTCCGCGAGGAAATGCGTATTTCAATTCAACGACATGAAACAGCGC	420							
Query 517	TTGACCAAGCTATTCATTTGTTGGCAGTCCAGAACTACAGAGTTCTCTTTGTCCGTG	576							
Db 421	CTGACACACCGCATCCCTCTGTTCCCGCGAGAACTACAGAGTCCCTCTGCTGACCGTG	480							
Query 577	TACGTTCAAGCAGCTAATCTTCACTCAGCGGCTTCGAGAGGTTAGCGTTTGGGCAA	636							
Db 481	TACGTTCAAGCAGCGGCAACTGCACTGAGCGTCTGCGGAGAGTCAAGCGTTTGGGCAA	540							
Query 637	AGGTGGGAGATTGATCTGCAACCATCAATTAACCGCTTACACGACCTTACAGCTGATT	696							

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OM nucleic search, using sw model

Run on: October 21, 2003, 04:41:07 ; Search time 5203 Seconds
(without alignments)
13023.425 Million cell updates/sec

Title: US-09-980-650-6
Perfect score: 2788
Sequence: 1 aaataagatcttactgttc.....taccagagatcataatcag 2788

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estopl.*
7: em_estro.*
8: em_estc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358.6	12.9	506	14	T24360
2	343.4	12.3	532	14	T15232
3	262	9.4	448	14	T14938
4	194	7.0	559	13	B082597

5	177.2	6.4	673	13	B0878720
6	171.8	6.2	255	13	BQ280286
7	167.8	6.0	686	13	B0893923
8	162	5.8	546	13	B0828900
9	161.6	5.8	551	13	B0828698
10	152.4	5.5	602	14	CA930016
11	151.6	5.4	600	13	B0826286
12	146	5.2	567	13	B0878721
13	140	5.0	659	14	CA929999
14	140	5.0	682	14	CA930552
15	133.6	4.8	588	14	B0827371
16	113.6	4.1	674	14	CA925612
17	107.6	3.9	314	14	CA929078
18	101.6	3.6	116	14	T14978
19	96.8	3.5	322	14	CA929990
20	94.4	3.4	576	14	CA929831
21	88.2	3.2	255	13	BQ280285
22	87.4	3.1	414	13	B0893847
23	85.2	3.1	675	13	BQ546804
24	83.2	3.0	603	12	B0120942
25	79.8	2.9	654	14	CD485177
26	75.8	2.7	628	14	CB329478
27	75.4	2.7	786	12	BP119110
28	73.4	2.6	819	12	BP119174
29	71.8	2.6	983	12	BG837559
30	71.2	2.6	312	12	BP119380
31	71	2.5	521	10	BG354049
32	70.6	2.5	179	14	CA929154
33	67.6	2.4	506	14	CA929067
34	65.6	2.4	494	9	AM746038
35	63.4	2.3	333	13	B0829081
36	63.4	2.3	383	10	BF586942
37	63.4	2.3	388	10	BF587479
38	61.4	2.2	629	12	BP118096
39	60.2	2.2	383	10	BF655880
40	59.6	2.1	554	12	BP118535
41	59.2	2.1	658	12	BP118003
42	59.2	2.1	662	12	BP118141
43	58.6	2.1	449	13	B0812453
44	58.2	2.1	630	12	BP117570
45	58.2	2.1	668	12	BP118481

ALIGNMENTS

RESULT 1
LOCUS T24360 506 bp mRNA linear EST 28-JUL-1995
DEFINITION crs1488 lambdaZAPST Ricinus communis cDNA clone pcrs1488, mRNA
SEQUENCE.
ACCESSION T24360
VERSION T24360.1 GI:689178
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; euroside I; Malpighiales; Euphorbiaceae; Ricinus.
REFERENCE 1 (bases 1 to 506)
vanderloo F.J., Turner S. and Somerville C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
JOURNAL Contact: Somerville CR
Carnegie Institution
Tel: 415351521
Email: cregandrew.stanford.edu
Seq primer: 73

FEATURES
source
Location/Qualifiers
1..506
/organism="Ricinus communis"
/mol_type="mRNA"

/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcrs1488"
/note="Vector: lambdaZAP11; Site 1: EcoRI; Site 2: XhoI; Poly(A)+ RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. CDNA was synthesized and cloned into lambdaZAP11 according to the instructions of the manufacturer (Stratagene); synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate."

BASE COUNT 143 a 97 c 119 g 142 t 5 others

ORIGIN

Query Match 12.9%; Score 358.6; DB 14; Length 506;
Best Local Similarity 87.0%; Pred. No. 2.9e-97;
Matches 440; Conservative 0; Mismatches 53; Indels 13; Gaps 4;

OY 1959 GTTGTATGATGCTGAGCCCTAGTGGTATGCGAATGCTATGTTGAT 2018
DB 1 GTTGTATGCTTCTGAGCCCTAGTGGTATGCGAATGCTATGTTGAT 60

OY 2019 GTTAGGATGAGATTCACACGGAACGCAATACATGTCGACATCTAT 2078
DB 61 GTTAGGATGAGATTCACACGGAACGCAATACATGTCGACATCTAT 120

OY 2079 ACAGATGCAATCAGCTCTGCACTTTGAAAAGAGCAATCTATTCATTAATGGAAG 2138
DB 121 ACAGATGCAATCAGCTCTGCACTTTGAAAAGAGCAATCTATTCATTAATGGAAG 180

OY 2139 TGTTTAATCTTACGGGTAGACGTCGGAGCTATGATGATGATGATGCAATCT 2198
DB 181 TGTTTAATCTTACGGGTAGACGTCGGAGCTATGATGATGATGATGCAATCT 240

OY 2199 GCTGCACTGATGCCACCGCTGCAATATGGAATGGAACCATGATTAATCCAGA 2258
DB 241 GCTGCACTGATGCCACCGCTGCAATATGGAATGGAACCATGATTAATCCAGA 300

OY 2259 TCTAGTCTAGTTTACGACGACATCAGGAACATGCTGACAC-TTACGGTGCAC 2317
DB 301 TCTAGTCTAGTTTACGACGACATCAGGAACATGCTGACAC-TTACGGTGCAC 360

OY 2318 CAACATTTATGCGCTTATGCA-----AGGTTGGCTTCTTATATATAT--TACACAC 2367
DB 361 CAACATTTATGCGCTTATGCA-----AGGTTGGCTTCTTATATATATAT--TACACAC 420

OY 2368 CTTTGTATCAAC--ATTGTTGGCTTATGCTGCTGCTTGCAGCAATATGAGCA 2425
DB 421 TTTTGTGCAACCCATTNGTTGGCTATATGCTGCTGCTTGCAGCAATATGAGCA 480

OY 2426 AGTATGATAGAGACTGTAGCAGTG 2451
DB 481 AAGTTGGATAGGCTGTAGAGTG 506

RESULT 2

LOCUS T15232 532 bp mRNA linear EST 28-JUL-1995
DEFINITION c18826 lambdaZAP11 Ricinus communis cDNA clone pcrs826 similar to agglutinin B chain, mRNA sequence.

ACCESSION T15232
VERSION T15232.1 GI:688885
KEYWORDS EST.
ORGANISM Ricinus communis (castor bean)
SOURCE Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; euroside 1; Malpighiales; Euphorbiaceae; Ricinus.
REFERENCE 1 (bases 1 to 532)
AUTHORS vandelaar, F.J., Turner, S. and Somerville, C.

TITLE
JOURNAL
COMMENT
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St., Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3.

FEATURES
source
1..532
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcrs826"
/note="Vector: lambdaZAP11; Site 1: EcoRI; Site 2: XhoI; Poly(A)+ RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. CDNA was synthesized and cloned into lambdaZAP11 according to the instructions of the manufacturer (Stratagene); synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate."

BASE COUNT 140 a 111 c 121 g 143 t 17 others

ORIGIN

Query Match 12.3%; Score 343.4; DB 14; Length 532;
Best Local Similarity 81.8%; Pred. No. 1.3e-92;
Matches 435; Conservative 0; Mismatches 88; Indels 9; Gaps 4;

OY 2193 AATCTGCTGCACTGATGCCACCGCTGCAATATGGAATGGAACCATATAT 2252
DB 1 AATCTGCTGCACTGATGCCACCGCTGCAATATGGAATGGAACCATATAT 60

OY 2253 CCCAGATCTAGTCTAGTTTACGACGACATCAGGAACAGTGTACACCTTACGGTG 2312
DB 61 CCCAGATCTAGTCTAGTTTACGACGACATCAGGAACAGTGTACACCTTACGGTG 120

OY 2313 CAACCAACATTTATGCGCTTATGCAAGTGTGCTTCTTATATATACCACTTTT 2372
DB 121 CAACCAACATTTATGCGCTTATGCAAGTGTGCTTCTTATATATATACCACTTTT 180

OY 2373 GTTACCAACATTTGCGCTTATGCTGCTGCTTGCAGCAATATGAGCAAGTATG 2432
DB 181 GTTACCAACATTTGCGCTTATGCTGCTGCTTGCAGCAATATGAGCAAGTATG 240

OY 2433 ATAGAGACTGTACAGTGAAGGCTGACACAGTGGCTCTTATGCAAGTGTCA 2492
DB 241 ATAGAGACTGTACAGTGAAGGCTGACACAGTGGCTCTTATGCAAGTGTCA 300

OY 2493 ATAGCTCTCAGCAACCGAGATAT--TTGCCCTTACAGAT--TCTATATACGG 2547
DB 301 ATAGCTCTCAGCAACCGAGATAT--TTGCCCTTACAGAT--TCTATATACGG 360

OY 2548 AAACAGTTGTAAGATCTCTCT--GTGGCCCTGACATCTCTGACCAACAGATGATTT 2605
DB 361 AAACAGTTGTAAGATCTCTCTCT--GTGGCCCTGACATCTCTGACCAACAGATGATTT 420

OY 2606 C--AAGATGATGGAACCATTTTAAATTTGTATAGTGTGTTAGATGAGGCGA 2663
DB 421 C--AAGATGATGGAACCATTTTAAATTTGTATAGTGTGTTAGATGAGGCGG 480

OY 2664 TCGATCGGACCTTAACAATATCTTACCTCTCCATGGAGCCCA 2715
DB 481 TCGATCGGACCTTAACAATATCTTACCTCTCCATGGAGCCCA 532

RESULT 3

LOCUS T14938 448 bp mRNA linear EST 28-JUL-1995

DEFINITION ccr424 lambdaZAPST Ricinus communis cDNA clone pcr424 similar to
ricin D chain B, mRNA sequence.
ACCESSION T14938
VERSION T14938.1 GI:688594
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
REFERENCE
1 (bases 1 to 448)
vanderloo, F.J., Turner, S. and Somerville, C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
JOURNAL Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CA 94305
Tel: 4153251521
Email: ccr@andrew.stanford.edu
Seq primer: T3.
Location/Qualifiers
1..448
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcr424"
/note="Vector: lambdaZAPST; Site 1: EcoRI; Site 2: XhoI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPST according
to the instructions of the manufacturer (Stratagene).
Synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."
BASE COUNT 118 a 81 c 92 g 140 t 17 others
ORIGIN
Query Match 9.4%; Score 262; DB 14; Length 448;
Best Local Similarity 96.4%; Pred. No. 7.3e-68;
Matches 268; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2488 GTTCAATACGCTCAGCAAAACGAGATAATGCTTACAAGTATTCTAATATACGG 2547
DB 1 GTTCAATACGCTCAGCAAAACGAGATAATGCTTACAAGTATTCTAATATACGG 60
QY 2548 AACAGTTGTAAGATCCTCTCTTGCGCCCTGCATCCTCTGGCCCAAGATGATGTC 2607
DB 61 AACAGTTGTAAGATCCTCTCTTGCGCCCTGCATCCTCTGGCCCAAGATGATGTC 120
QY 2608 AGAATGATGAAACCAATTTTAAATTTGTAAGTGGTGTGTAATGATGAGGCGATCGG 2667
DB 121 AGAATGATGAAACCAATTTTAAATTTGTAAGTGGTGTGTAATGATGAGGCGATCGG 180
QY 2668 ATCCGAGCTTAAACCAATCATTTCTTACCCCTGCATGATGATGCCAAACCAATATGAT 2727
DB 181 ATCCGAGCTTAAACCAATCATTTCTTACCCCTGCATGATGATGCCAAACCAATATGAT 240
QY 2728 TACCATTAATTTGATAGACAGATTACAAGCTTGTGAG 2765
DB 241 TACCATTAATTTGATAGACAGATTACTCTCTTGACAGTG 278
RESULT 4
LOCUS BU825997 559 bp mRNA linear EST 15-OCT-2002
DEFINITION UK115TE03 Populus apical shoot cDNA library Populus tremula x
Populus tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION BU825997
VERSION BU825997.1 GI:23998128

KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
1 (bases 1 to 559)
Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
JOURNAL Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
1..559
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="apical shoot"
/clone_id="Populus apical shoot cDNA library"
BASE COUNT 168 a 123 c 122 g 146 t
ORIGIN
Query Match 7.0%; Score 194; DB 13; Length 559;
Best Local Similarity 59.4%; Pred. No. 4.3e-47;
Matches 329; Conservative 0; Mismatches 225; Indels 0; Gaps 0;
QY 1933 GCTGAGTACTGAGAATTCATGCTGATGTTGTATGATCTGACCCCATGATGCGTATCG 1992
DB 6 GCCCTGCGGCCAAGAAATGACATGTTGTTCTGTTCAAAATCCACACACATCATG 65
QY 1993 TAGGTCAATGCTCTATGTTGTTATGTTAGTGAATGGAATTCACACAGGAACGCA 2052
DB 66 TTGGCATTAATAATTTTGGCGTTGACGTGTTCTTGAACCTTACTTTGATGAAACTTAG 125
QY 2053 TACAGTTGGCCATGCAAGCTTAATACAGATGCAATTCAGCTCTGAGCTTTGAAAGAG 2112
DB 126 TACAGTTGACCCGTGTAATCTTAACGAGATGTAATCAACATGAGAGCTTGAGAGA 185
QY 2113 ACAATACTATTCGATCTTAATGGAAGTGTTTAATCTTAACGAGTCCGAGACT 2172
DB 186 ACGAATCATTCATCTTAAGGCAAGTGTGGCCACAAAGGCAAGTCCAGAGAGCT 245
QY 2173 ATGTGATGATTTATGATTTGCAATCTGCTGCAATGATGCCACCCGCTGCAATATG 2232
DB 246 ATGTGATGATTTATGATTTGCAATCTGCTGCAAGGTAAGGCTAGGCGCCCAATTTG 305
QY 2233 ATTAATGAAACCATTAATATCCGATCTAGTTTATGACGCGCATCAGGAACA 2292
DB 306 AGAATGGCTCATCTTAACCCCTCTGCTGCTAGTTTATGACCTCAAAAGTCAAGGAAA 365
QY 2293 GTGTACCACTTACGCTGCAACCAATTTATGCGGTAGTCAAGTTGGCTTCTTA 2352
DB 366 GTGTGCTCTACTCACCCTTGAAACCAATGTTATGCTTGGGCAAGAGATGGGCTTTCA 425
QY 2353 CTAAATATACCAACCTTTTGTACACCAATTTGTTGGCTATATGTTGCTTGCAG 2412
DB 426 CCGATGTTTCAAAACCAACCAAGAGTCAATGTCGGGCTTTGGAGTACTGCTTGAAT 485
QY 2413 CAATATGAGCAAGATGATGATAGAGCTGTACAGAGTAAGAAAGCTGAAACAAGTGGG 2472
DB 486 TTAACAATATGTCCTCAAAAGTTAGCAAGTGCCTGAGAGAACAGACTGAACAATTA 545
QY 2473 CTCTTTATGACAT 2486
DB 546 ATTTTACGACAT 559

RESULT 5
 BUB878720 673 bp mRNA linear EST 16-OCT-2002
 LOCUS V050F06 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.
 DEFINITION BUB878720
 ACCESSION BUB878720.1 GI:24070244
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Populus balsamifera subsp. trichocarpa
 Populus balsamifera subsp. trichocarpa
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 673)
 1 (bases 1 to 673)
 Uneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
 JOURNAL
 TITLE
 AUTHORS
 COMMENT
 Unpublished
 Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
 source
 1. .673
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"
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BASE COUNT 200 a 141 c 152 g 180 t

ORIGIN

Query Match 6.4%; Score 177.2; DB 13; Length 673;
 Best Local Similarity 60.3%; Pred. No. 6.4e-42;
 Matches 293; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 1933 GCTAGTACTGAGATTTCATCTGATGTTGATGAGATCCGAGCCCATAGGCTATCG 1992
 DB 184 GCTGTCGTCGCAAAAATGACGATGTTGTTCTGTTCAAGTCCACACACATG 243
 QY 1993 TAGGTGCAATGCTATGTTGTTAGGATGGAAGATCCACAACGGAACGCA 2052
 DB 244 TTGGCATTAATATTGTCGTTGCGTTGCTTGAATCTACTTTGATAAAACATAG 303
 QY 2053 TACAGTTGGCCATGCAAGTCTAATACAGATGCAATCAGCTTGAAGAAAGAG 2112
 DB 304 TACAGTTGACCCCGTAAATCTGACGAGATGTGAAATCAACAATGAGAGTTGAGAGA 363
 QY 2113 ACAATACATTCGATCTAATGAAAGTTTAACTAATGAGGATCCGAGGAGCT 2172
 DB 364 ACGAATCATTCATTAAGGCAAGTTTGACCAACAACGCAAGTCCAGGAAGT 423
 QY 2173 ATGTGATGATCTATGATGCAATATCTGTCGCAACTGATGCCACCCGCTGGCAATATG 2232
 DB 424 ATGTATTATCTGTCGTCGCAACAAGTGAAGGCTAAGGCCCAATTTGAAAGTACAA 483
 QY 2233 ATATGGAACCATCTAATAATCCAGATCTAGTCTAGTTTACGACGACATCAGGAACA 2292
 DB 484 AGGATGGCTCATCTTAACCCCTCTGTCATGATTTGACCTCAAAAGTCGGGGA 543
 QY 2293 GTGGTACACACTTACGGTGCAACCAATTTATGCGCTTATGTCAGGTTGGCTTCTTA 2352
 DB 544 GTGGCTCCCTACTACCTTGGAACCAATGTTAGCCTTGGCCCAAGTTGGAATTTCA 603
 QY 2353 CTAAATATACACACCTTTTGTACCAACCATGTTGGGCTATATGCTGTGCTTGAAG 2412
 DB 604 CCAAGTGTTCAAAAACCATCACCAAGTGCATTTGTGGGGCTTGGGGCTACTGCTTGAT 663
 QY 2413 CAAATA 2418

DB 664 TTAAACA 669

RESULT 6
 BQ280286 255 bp mRNA linear EST 01-MAY-2003
 LOCUS PAC000000001474 Pioneer Af-1 array Zea mays cDNA, mRNA sequence.
 DEFINITION BQ280286
 ACCESSION BQ280286
 VERSION BQ280286.1 GI:30270760
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Zea mays
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 255)

REFERENCE
 Habben, J.
 Analysis of gene expression in drought stressed maize
 JOURNAL
 TITLE
 AUTHORS
 COMMENT
 Unpublished
 Contact: Habben J
 Trait and Technology Development, Agronomic Traits
 Pioneer Hi-Bred International, Inc.
 7250 NW 62nd Ave., P.O. Box 552, Johnston, IA 50131-0552, USA
 Tel: 515 270 4130
 Fax: 515 334 4778
 Email: jefirey.habben@pioneer.com.

FEATURES
 source
 1. .255
 /organism="Zea mays"
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 /clone_id="Pioneer Af-1 array"

BASE COUNT 47 a 93 c 65 g 50 t

ORIGIN

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 Best Local Similarity 79.6%; Pred. No. 1.6e-40;
 Matches 203; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 97 ATGACAAACCAACCAACATCAAGAAATGATTCATTCATCACTGAGTATACCA 156
 DB 1 ATGACAAACCAACCAACATCAAGAAATGATTCATTCATCACTGAGTATACCA 60
 QY 157 GTTAAGTACTTGGTGAAGAACGATTAACCGGTTACATCTCCCATGACATCTCTTG 216
 DB 61 GTGAGGTCGTCGGGGGAGCGATCGAAGCCGGCTACACCCGATGACATCTCCCTC 120
 QY 217 TCTTTGACACAGTTTCTGCTAGCGAGTTCGTGCCAGTCTGGGTTGTTCTGGACTA 276
 DB 121 TCCCTCACCCAGTTCCTCTCTCCGAGTTCTGTCAGGCGCGGCTTGCTGCTGGCTC 180
 QY 277 GTTGACATCATCTGGGGATCTTTGTCATCTCAATGAGATTCCTGGTGAAT 336
 DB 181 GTGACATCATCTGGGGATCTTTGCGCCGCTCCAGTGGAGCGCTTCTGTCGAGATC 240
 QY 337 GAGCAGTTGATCAAC 351
 DB 241 GAGCAGTTAATTAAC 255

RESULT 7
 BUB93923 686 bp mRNA linear EST 17-OCT-2002
 LOCUS P084E06 Populus petioles cDNA library Populus tremula cDNA 5 prime, mRNA sequence.
 DEFINITION BUB93923
 ACCESSION BUB93923.1 GI:24104988
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Populus tremula
 Populus tremula
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 686)	Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.	The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries	Unpublished	
	Contact: BHALERAO RUPALI R.	Umea Plant Science Center		
	Department of Plant Physiology			
	University of Umea, 901 87 Umea, Sweden			
	Tel: +46 90 786 5279			
	Fax: +46 90 786 6676			
	Email: rupali.bhalerao@planphys.umu.se.			
FEATURES				
source				
	1. 686			
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	/db_xref="taxon:113616"			
	/issue_type="petioles"			
	/clone_lib="Populus petioles cDNA library"			
BASE COUNT	197 a 149 c 161 g 178 t			1 others
ORIGIN				
Query Match	6.0%; Score 167.8; DB 13; Length 686;			
Best Local Similarity	60.8%; Pred. No. 4.7e-39;			
Matches 291; Conservative 0; Mismatches 187; Indels 1; Gaps 1;				
Oy	1933 GCTGAGTACTGAGAAATTCATCTGTAAGTGTTCATAGATCTCGAGCCCATAGTGGCTATGC			1992
Db	209 GCTCTGTCGTCGCAAAAATATACATGTGTTGTTCTGGTGCAGAAAGTCCACACACATGTG			268
Oy	1993 TAGGTGCAATGCTCTATGTGTGATGTTAAGGATGGAAGATTCACACGGAAGCCAA			20522
Db	269 TTGGCATTAATAATTTGTGCGTTGACGCTGTTCTTGAACCTACTAGATGGAAGACGTAG			328
Oy	2053 TACAGTGTGGCCATGCAAGTCTAATACAGATGCAATACAGCTCTGACCTTGGAAAAGAG			2112
Db	329 TACAGTGTACCCGCTGAATCTAACGGAATGGAATCAACAATGAGCTTGGAGAAGA			388
Oy	2113 ACAATACTATTGATCTAATAGGAAGTGTTTAACTACTTACGGGTACAGTCCGGAGTCT			21722
Db	389 ACGGACCATTCATCAATCTAAGAAAGTGTTTGGCAACAAACGGCAACAGTCCAGGAAGCT			448
Oy	2173 ATGTGATGATCTAATGATTTGCAATACTGCTGCAACTGATGCCACCCGCTGGCAATATGCG			2232
Db	449 ATGATATTTATCTCGACGCAACAAAGGAGGCTAGGCCACAAATTTGGAAGATGACAA			508
Oy	2233 ATAAATGGAACCATCATTAATCCAGATTTAGTCTAGTTTATAGCAGCAGCATCAGGAAAC			22922
Db	509 AGGATGGCTCATCCTTAACCCCTCCTGTCATAGTTTGAACCTCAAAAGTCGGGAAAA			568
Oy	2293 GTGTACCACTTAAGGTGCAACCAACATTTATGCGCTTAATGTCAGAGTTGGCTTCTTA			23522
Db	569 GTGGTCTCCCTACTGAC-CTGGGAACCAATGTTTATGCTTGGGCCCAAGTTGGAAATTTCA			627
Oy	2353 CTAATTAATACCAACCTTTGTGTAACCACTTTGTGGGCTATATAGTGTGTCGTTGCA			2411
Db	628 CCAAGTCTTCAAAACCATCACCGAAGTCCATTTGCGGAGCTTTGGGACTACTGCTTGGAA			686
RESULT 8				
BUS28900	546 bp	mRNA	linear	EST 15-OCT-2002
LOCUS	K03084P	Populus apical shoot cDNA library	Populus tremula x	
DEFINITION	Populus tremuloides cDNA 5 prime, mRNA sequence.			
ACCESSION	BUS28900			
VERSION	BUS28900.1	GI:24004289		
KEYWORDS	EST.			
SOURCE	Populus tremula x Populus tremuloides			
ORGANISM	Populus tremula x Populus tremuloides			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; rosids			
	; euroside 1; Malpighiales; Salicaceae; Populus.			

FEATURES	source
JOURNAL	Unpublished
AUTHORS	1 (bases 1 to 546)
TITLE	Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
COMMENT	The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
CONTACT	Unpublished
CONTACT	Contact: BHALERAO RUPALI R.
CONTACT	Umea Plant Science Center
CONTACT	Department of Plant Physiology
CONTACT	University of Umea, 901 87 Umea, Sweden
CONTACT	Tel: +46 90 786 6679
CONTACT	Fax: +46 90 786 6676
CONTACT	Email: rupali.bhalerao@janephy.su.se.
LOCATION	Location/Qualifiers
FEATURES	1. 546
FEATURES	/organism="Populus tremula x Populus tremuloides"
FEATURES	/mol_type="mRNA"
FEATURES	/db_xref="taxon:47664"
FEATURES	/cbase_type="apical shoot"
FEATURES	/clone_id="Populus apical shoot cDNA library"
BASE COUNT	154 a 124 c 125 g 143 t
ORIGIN	
Query Match	5.8% Score 162; DB 13; Length 546;
Best Local Similarity	58.2%; Pred. No. 2.4e-37;
Matches 313; Conservative	0; Mismatches 210; Indels 15; Gaps 1;
Db	2155 GGTACAGTCCGGAGTCTATGTGTATGATCTATGATTTGCAATACCTGCTGCAACTGATGCCA 2214
Db	6 GGACAAAGTCAAGAAAGTATGATTTATCTCTGACTCCAAACAGGTAAAGGCTAGCCCA 65
Db	2215 CCCGCTGGCAATATGGATTAATGAAACCATCATTAATCCCAAGTCTAAGTCTAATTTTGA 2274
Db	66 CAATTTGGAAAGTCAAAAGAGATGGCTCCATCTCAACCCCTCTCATATTTTGA 125
Db	2275 CAGGCAATCAAGGAAACAGTGTATCCACACTTACGCTGCAAAACCAATTTATCCGTTA 2334
Db	126 CTTAAAGTCGGGAAAGTGTGCTCTCTACTCTACCTTGGAACCAATGTTATCCCTTGG 185
Db	2335 GTCAAGGTGGCTTCTACTAATTAATACACAACCTTTTGTTCACCAATGTTGGGCTAT 2394
Db	186 GCCAAGGTGGAAATTTTACACAGTGTTCACAAACCATCAACGAACTCATGTGCGGCTTT 245
Db	2395 ATGCTGTGCTTCACAGCAAAATGTGGAACAAGTATGATGATGAGAGCTGTGACAGTGA 2454
Db	246 GGGACTACTGCTTGAATTTTACAAAAAGGCTCCAAAGTTAGCCAAAGTGTGGAAGACA 305
Db	2455 AGGCTGAACAACAGTGGGCTCTTTATGACAGTGTCAATACGTCCTACGAAACCGAG 2514
Db	306 AGACTGAACAAAAATGAAATCTTACCCCGAGTGTGATGATGATGATGATGATGATGATG 365
Db	2515 ATATTTGCTTACAGATGATCTTAATATAGCGGAAACAGTTGTTAAGTCTCTCTGTG 2574
Db	366 ATTGTGTCTACTAGCATGAAATACCAAGAAAGTCTGCTCTGTTCTCTCTGTA 425
Db	2575 GCCCTGCATCCTCTGCGCAACGATGATGTT-----CAAGATGAGAA 2619
Db	426 GCCCTGTGATCTTAACCAAGTGTGGAAGTTGGGACAGCAGCGCAACGATATTTCC 485
Db	2620 CCAATTTTAATTTGATATGATGATTTGTTGATGATGAGGCGATCGATCCGAGCT 2677
Db	486 CCAATTTTGAACGTGAATATATGCTTTGTGTGTGATGTGAGCTATTCATCTTAACTT 543
RESULT 9	
LOCUS	BUS28698 551 bp mRNA linear EST 15-OCT-2002
DEFINITION	K02695P Populus apical shoot cDNA library Populus tremula x
ACCESSION	BUS28698
VERSION	BUS28698.1 GI:24003857
KEYWORDS	EST.
SOURCE	Populus tremula x Populus tremuloides
ORGANISM	Populus tremula x Populus tremuloides

RESULT 11
BU826286 600 bp mRNA linear EST 15-OCT-2002
LOCUS BU826286
DEFINITION U118G11 Populus apical shoot cDNA library Populus tremula x
Populus tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION BU826286
VERSION BU826286.1 GI:23998729
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
/ eucosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 600)
AUTHORS Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
JOURNAL Unpublished
COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
source 1. .600
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/issue_type="apical shoot"
/clone_lib="Populus apical shoot cDNA library"
BASE COUNT 181 a 125 c 132 g 158 t
ORIGIN

Query Match 5.4%; Score 151.6; DB 13; Length 600;
Best Local Similarity 61.3%; Pred. No. 3.7e-34;
Matches 244; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 1933 GCTAGTCTGAGAAATTCATGCTGATGTTTGTATGATCCGAGCCCATAGGCTATCG 1992
DB 203 GCCCTGTCGCCAAGAAATGACGATGTTTCTGTTCAAGTCCACACACATTTG 262
QY 1993 TAGGTGCAATGCTCTATGTTGTTAGGATGAGATTCACACGGAACGCA 2052
DB 263 TTGGCATTAATTAATTTGTCGCTGACGTTCTTGAATCTACTTTGATGAACTTAG 322
QY 2053 TACAGTTGTGGCCATGCAAGTCTTAATACAGATGCAATCACTGCTTGAAGAG 2112
DB 323 TACAGTTGACCCGCTGAATCTTAACGAGATGTAATCAACATGAGAGCTTGAGAGA 382
QY 2113 ACAATACTATTGATCTAATGAAAGTGTAACTTAACCTTACGCGGTACAGTCCGAGCT 2172
DB 383 ACGGAACCATTAATCTAAGGCAAGTGTGGCCACAAAGGCAAGTCCAGAGACT 442
QY 2173 ATGTGATGATCTATGATGCAATAGTCTGCAACTGATGACCCGCTGCGCAATATGSG 2232
DB 443 ATGTATTATCTCTGACGCAACAGTGGAAGGCTTAGGCCCATTTGAAAAATACAA 502
QY 2233 AATAATGAAACCATTAATATCCAGATCTAGTCTAGTTTACGACGACATAGGAAACA 2292
DB 503 AGGATGGCTCATCTTAAGCCCTCTGCTGACTGTTTGAACCTCAAGTCAAGGAGAAA 562
QY 2293 GTGTACCAACCTTACGGTGCAACCAATTTATGCC 2330
DB 563 GTGGCTCCCTACTCCTTGAAACCAATGTTATGCC 600

RESULT 12
BU878721 567 bp mRNA linear EST 16-OCT-2002
LOCUS BU878721
DEFINITION V050F07 Populus flower cDNA library Populus balsamifera subsp.

ACCESSION BU878721
VERSION BU878721.1 GI:24070245
KEYWORDS EST.
SOURCE Populus balsamifera subsp. trichocarpa
ORGANISM Populus balsamifera subsp. trichocarpa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
/ eucosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 567)
AUTHORS Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
JOURNAL Unpublished
COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
source 1. .567
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
BASE COUNT 174 a 119 c 129 g 145 t
ORIGIN

Query Match 5.2%; Score 146; DB 13; Length 567;
Best Local Similarity 60.7%; Pred. No. 1.8e-32;
Matches 239; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1933 GCTGAGTCTGAGAAATTCATGCTGATGTTTGTATGATCTGAGCCCATAGGCTATCG 1992
DB 174 GCTCTGTCGCCAAGAAATGACGATGTTTCTGTTCAAGTCCACACACATTTG 233
QY 1993 TAGGTGCAATGCTCTATGTTGTTAGGATGAGATTCACACGGAACGCA 2052
DB 234 TTGGCATTAATTAATTTGTCGCTGACGTTCTTGAATCTACTTTGATGAACTTAG 293
QY 2053 TACAGTTGTGGCCATGCAAGTCTAATACAGATGCAATCACTGCTTGAAGAG 2112
DB 294 TACAGTTGACCCGCTGAATCTTAACGAGATGTAATCAACATGAGAGCTTGAGAGA 353
QY 2113 ACAATACTATTGATCTAATGAAAGTGTAACTTAACCTTACGCGGTACAGTCCGAGCT 2172
DB 354 ACGGAACCATTAATCTAAGGCAAGTGTGGCCACAAAGGCAAGTCCAGAGACT 413
QY 2173 ATGTGATGATCTATGATGCAATAGTCTGCAACTGATGACCCGCTGCGCAATATGSG 2232
DB 414 ATGTATTATCTCTGACGCAACAGTGGAAGGCTTAGGCCCATTTGAAAAATACAA 473
QY 2233 AATAATGAAACCATTAATATCCAGATCTAGTCTAGTTTACGACGACATAGGAAACA 2292
DB 474 AGGATGGCTCATCTTAAGCCCTCTGCTGACTGTTTGAACCTCAAGTCCGAGAGAAA 533
QY 2293 GTGTACCAACCTTACGGTGCAACCAATTTA 2326
DB 534 GTGGCTCCCTACTCCTTGAAACCAATGTTTA 567

RESULT 13
CA929999 659 bp mRNA linear EST 30-DEC-2002
LOCUS CA929999
DEFINITION MT02CA.P5.G01 Aspen apex cDNA library Populus tremuloides cDNA,
mRNA sequence.
ACCESSION CA929999
VERSION CA929999.1 GI:27418480
KEYWORDS EST.

SOURCE
ORGANISM Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 659)
REFERENCE Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
AUTHORS C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
FEATURES
source 1..659
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA library"
/note="Organ: apex"
BASE COUNT 188 a 144 c 139 g 188 t
ORIGIN
Query Match 5.0%; Score 140; DB 14; Length 659;
Best Local Similarity 58.1%; Pred. No. 1.3e-30;
Matches 294; Conservative 0; Mismatches 195; Indels 17; Gaps 2;
QY 2236 ATGGAACCATATTAATCCAGATCTAGTCTAGTTTTCAGACGACATCAGGGAACAGTG 2295
DB 7 ATGGCTCATCTTAACCCCTCCTCGTCACTAGTTTACCTCAAGTCGGGGAATG 66
QY 2296 GTACCACTTACGCTGCAAAACCAATTATGCCGTTAGTCAGCTTGCTCTACTA 2355
DB 67 GCTCCCTCCTACCTTGGAACCAATGTTATGCTTGCGCCAGGTTGGAATTCACCA 126
QY 2356 ATTAATACCAACCTTTTTCACACATGTTGGGCTATATGCTGCTTTCAGACAA 2415
DB 127 GTGTTTCAAAACCATCCAGAGTCATGTCGGGCTTGGAGCTACTGCTTGAAATTTA 186
QY 2416 ATAGTGACAAGTATGATAGAGACTGAGCACTGAAAGGCTGAAACAACAGTGGCTC 2475
DB 187 ACAAAAAGGTCCCAAAAGTTAGCCAGTGGTGAAGAACAAGCTGAACAAAATGGAATT 246
QY 2476 TTTATGCAAGTGTTCATACCTCTCAGCAAAACCGAGATTAATGCTTACAGTATT 2535
DB 247 TTTACGC--ATGGTTCGATAGAGGTTGGTCMAACAGATTGTCCTTAACCTACGATG 304
QY 2536 CTAATATACGGGAACAGTGTTAAGATCCTCTTGTGGCCCTGCATCCTGGCCAC 2595
DB 305 GAAATACCAAAAGAGCTTGTCGTCGTTGTCCTTGAGCCCTGTCATTAACCAAC 364
QY 2596 GATGATGTT-----CAAGATGATGAACATTTTAATTTGTAATG 2640
DB 365 GTTGACGTTTGGGGAACAGCCAGGCAAGCTATTTCCTTTGAACGTAATATG 424
QY 2641 GATTGCTTTAGATGTGAGCGATCGATCCGAGCTTAACAATCATTTTACCCTC 2700
DB 425 CTTTGCTTTGATGTGAGCTATTCATCTTAACCTTTTCAAAATAATTATTGGGATT 484
QY 2701 TCCATGTGACCAACCAAAATATGG 2726
DB 485 TCAACGAGAGACTTAACGATATGG 510

RESULT 14
CA930552 692 bp mRNA linear EST 30-DEC-2002
LOCUS CA930552/c
DEFINITION MTUCA.P23.H10 Aspen apex cDNA library Populus tremuloides cDNA,

ACCESSION mRNA sequence.
CA930552
VERSION CA930552.1 GI:27419032
KEYWORDS EST.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 692)
REFERENCE Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
AUTHORS C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
FEATURES
source 1..692
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA library"
/note="Organ: apex"
BASE COUNT 199 a 147 c 153 g 193 t
ORIGIN
Query Match 5.0%; Score 140; DB 14; Length 692;
Best Local Similarity 58.1%; Pred. No. 1.4e-30;
Matches 294; Conservative 0; Mismatches 195; Indels 17; Gaps 2;
QY 2236 ATGGAACCATATTAATCCAGATCTAGTCTAGTTTTCAGACGACATCAGGGAACAGTG 2295
DB 688 ATGGCTCATCTTAACCCCTCCTCGTCACTAGTTTTCAGCTCAAGTCGGGGAATG 629
QY 2296 GTACCACTTACGCTGCAAAACCAATTATGCCGTTAGTCAGAGTTGCTCTACTA 2355
DB 628 GCTCCCTCCTACCTTGGAACCAATGTTATGCTTGCGCCAGGTTGGAATTCACCA 569
QY 2356 ATTAATACCAACCTTTTTCACACATGTTGGGCTATATGCTGCTTTCAGACAA 2415
DB 568 GTGTTTCAAAACCATCCAGAGTCATGTCGGGCTTGGGACTACTGCTTGAATTTA 509
QY 2416 ATAGTGACAAGTATGATAGAGACTGAGCACTGAAAGGCTGAAACAACAGTGGCTC 2475
DB 508 ACAAAAAGGTCCCAAGTTAGCCAGTGGTGAAGAACAAGCTGAACAAAATGGAATT 449
QY 2476 TTTATGCAAGTGTTCATACCTCTCAGCAAAACCGAGATTAATGCTTACAGTATT 2535
DB 448 TTTACGC--ATGGTTCGATAGAGGTTGTCGTAACACAGATTTGCTTAACAGCATG 391
QY 2536 CTAATATACGGGAACAGTGTTAAGATCCTCTTGTGGCCCTGCATCCTGGCCAC 2595
DB 390 GAAATACCAAAAGAGCTTGTCGTCGTTGTCCTTGAGCCCTGTCATTAACCAAC 331
QY 2596 GATGATGTT-----CAAGATGATGAACATTTTAATTTGTAATG 2640
DB 330 GTTGACGTTTGGGGAACAGCCAGGCAAGCTTATTTCCCATTTTGAACGTAATATG 271
QY 2641 GATTGCTTTAGATGTGAGCGATCGATCCGAGCTTAACAATCATTTTACCCTC 2700
DB 270 CTTTGCTTTGATGTGAGCTATTCATCTTAACCTTTTCAAAATAATTATTGGGATT 211
QY 2701 TCCATGTGACCAACCAAAATATGG 2726
DB 210 TCAACGAGAGACTTAACGATATGG 185

RESULT 15
BU827371

LOCUS BU827371 588 bp mRNA linear EST 15-OCT-2002
DEFINITION UK131TH03 Populus apical shoot cDNA library Populus tremula x
Populus tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION BU827371
VERSION BU827371.1 GI:24001037
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eustosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 588)
Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished

REFERENCE 1 (bases 1 to 588)
Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
JOURNAL COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
SOURCE 1. 588
Location/Qualifiers
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="apical shoot"
/clone_lib="Populus apical shoot cDNA library"

BASE COUNT 176 a 128 c 130 g 154 t
ORIGIN

Query Match 4.8%; Score 133.6; DB 13; Length 588;
Best Local Similarity 60.4%; Pred. No. 1.1e-26;
Matches 220; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
QY 1933 GCTGAGTACTGAGAATTCATGCTGATGTTTGTATGATCCTGAGCCCATAGTGCCTATCG 1992
DB 209 GCCCTGCTGTCGAAGAATGACGATGTTGTTTCGTTCAAGTCCACACACACATG 268
QY 1993 TAGTCGAATGCTCTATGTTGTTGATGTTAGGATGGAAGATTCCACAACGGAACGCA 2052
DB 269 TTGCGATTAATTAATTTGCGCTGACGCTTCTTGAACCTACTTGTGATGAAACTTAG 328
QY 2053 TACAGTTGCGCATGCAAGCTAATACAGATGCAATCAGCTCTGACCTTGAAGAG 2112
DB 329 TACAGTTGACCCGTTAATCTAAGGAGATGTAATCAACAATGAGCTTGGAGAGA 388
QY 2113 ACAATACTATTGATCTAATGAGAAAGTTTAATTAATTAATTAATTAATTAATTAATTAAT 2172
DB 389 ACGGAAACCATTCATCTTAAGGCAAGTGTGGCCACAACGCAACAGTCCAGGAAGCT 448
QY 2173 ATGTGATGATCTAATGATGCAATACTGCTGCAACTGATGCCACCCGCTGCAAAATATGGG 2232
DB 449 ATGTATTATCTGACGCAACAAAGTGGAAGGCTAGCGCCACAATTTGAAAAATACAA 508
QY 2233 ATATGGAACCATTAATCCAGATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2292
DB 509 AGAATGCTCATCTTAACCCCTCTGTCACCTAGTTTGAACCTCAAAATGACGGAATA 568
QY 2293 GTGG 2296
DB 569 GTGG 572

Search completed: October 21, 2003, 06:57:50
Job time : 5209 secs